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(21) International Application Number: PCT/AU99/00195		(AU). RICE, Robert, Norman [AU/AU]; 39 Foley Place, Sinnamon Park, QLD 4073 (AU).	
(22) International Filing Date: 19 March 1999 (19.03.99)		(74) Agents: HUGHES, E., John, L. et al.; Davies Collison Cave, 1 Little Collins Street, Melbourne, VIC 3000 (AU).	
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(71) Applicants (for all designated States except US): AG-GENE AUSTRALIA LIMITED [AU/AU]; Level 4, 62 Pitt Street, Sydney, NSW 2000 (AU). STATE OF QUEENSLAND through its DEPARTMENT OF PRIMARY INDUSTRIES [AU/AU]; Primary Industries Building, 80 Ann Street, Brisbane, QLD 4000 (AU).			
(72) Inventors; and (75) Inventors/Applicants (for US only): GRAHAM, Michael, Wayne [AU/AU]; 42 Raglan Street, St. Lucia, QLD 4076			
(54) Title: CONTROL OF GENE EXPRESSION			
(57) Abstract			
<p>The present invention relates generally to a method of modifying gene expression and to synthetic genes for modifying endogenous gene expression in a cell, tissue or organ of a transgenic organism, in particular a transgenic animal or plant. More particularly, the present invention utilises recombinant DNA technology to post-transcriptionally modify or modulate the expression of a target gene in a cell, tissue, organ or whole organism, thereby producing novel phenotypes. Novel synthetic genes and genetic constructs which are capable of repressing delaying or otherwise reducing the expression of an endogenous gene or a target gene in an organism when introduced thereto are also provided.</p>			

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## CONTROL OF GENE EXPRESSION

### FIELD OF THE INVENTION

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of a transgenic organism, in particular a transgenic animal or plant. More particularly,  
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thereto are also provided.

### GENERAL

15 Bibliographic details of the publications referred to in this specification are collected at  
the end of the description.

As used herein the term "derived from" shall be taken to indicate that a specified  
integer may be obtained from a particular specified source or species, albeit not  
20 necessarily directly from that specified source or species.

Throughout this specification, unless the context requires otherwise, the word  
"comprise", or variations such as "comprises" or "comprising", will be understood to  
imply the inclusion of a stated step or element or integer or group of steps or elements  
25 or integers but not the exclusion of any other step or element or integer or group of  
elements or integers.

Those skilled in the art will appreciate that the invention described herein is susceptible  
to variations and modifications other than those specifically described. It is to be  
30 understood that the invention includes all such variations and modifications. The

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invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations or any two or more of said steps or features.

- 5 The present invention is not to be limited in scope by the specific embodiments described herein, which are intended for the purposes of exemplification only. Functionally-equivalent products, compositions and methods are clearly within the scope of the invention, as described herein.
- 10 Sequence identity numbers (SEQ ID NOS.) containing nucleotide and amino acid sequence information included in this specification are collected after the Abstract and have been prepared using the programme PatentIn Version 2.0. Each nucleotide or amino acid sequence is identified in the sequence listing by the numeric indicator <210> followed by the sequence identifier (e.g. <210>1, <210>2, etc). The length, type 15 of sequence (DNA, protein (PRT), etc) and source organism for each nucleotide or amino acid sequence are indicated by information provided in the numeric indicator fields <211>, <212> and <213>, respectively. Nucleotide and amino acid sequences referred to in the specification are defined by the information provided in numeric indicator field <400> followed by the sequence identifier (eg. <400>1, <400>2, etc).

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The designation of nucleotide residues referred to herein are those recommended by the IUPAC-IUB Biochemical Nomenclature Commission, wherein A represents Adenine, C represents Cytosine, G represents Guanine, T represents thymine, Y represents a pyrimidine residue, R represents a purine residue, M represents Adenine 25 or Cytosine, K represents Guanine or Thymine, S represents Guanine or Cytosine, W represents Adenine or Thymine, H represents a nucleotide other than Guanine, B represents a nucleotide other than Adenine; V represents a nucleotide other than Thymine, D represents a nucleotide other than Cytosine and N represents any nucleotide residue.

30

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The designation of amino acid residues referred to herein, as recommended by the IUPAC-IUB Biochemical Nomenclature Commission, are listed in Table 1.

TABLE 1

	Amino Acid	Three-letter code	One-letter code
	Alanine	Ala	A
	Arginine	Arg	R
	Asparagine	Asn	N
5	Aspartic acid	Asp	D
	Cysteine	Cys	C
	Glutamine	Gln	Q
10	Glutamic acid	Glu	E
	Glycine	Gly	G
15	Histidine	His	H
	Isoleucine	Ile	I
	Leucine	Leu	L
	Lysine	Lys	K
	Methionine	Met	M
20	Phenylalanine	Phe	F
	Proline	Pro	P
	Serine	Ser	S
	Threonine	Thr	T
	Tryptophan	Trp	W
25	Tyrosine	Tyr	Y
	Valine	Val	V
	Aspartate/Asparagine	Baa	B
	Glutamate/Glutamine	Zaa	Z
	Any amino acid	Xaa	X

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## BACKGROUND TO THE INVENTION

Controlling metabolic pathways in eukaryotic organisms is desirable for the purposes of producing novel traits therein or introducing novel traits into a particular cell, tissue or organ of said organism. Whilst recombinant DNA technology has provided 5 significant progress in an understanding of the mechanisms regulating eukaryotic gene expression, much less progress has been made in the actual manipulation of gene expression to produce novel traits. Moreover, there are only limited means by which human intervention may lead to a modulation of the level of eukaryotic gene expression.

10

One approach to repressing, delaying or otherwise reducing gene expression utilise a mRNA molecule which is transcribed from the complementary strand of a nuclear gene to that which is normally transcribed and capable of being translated into a polypeptide. Although the precise mechanism involved in this approach is not 15 established, it has been postulated that a double-stranded mRNA may form by base pairing between the complementary nucleotide sequences, to produce a complex which is translated at low efficiency and/or degraded by intracellular ribonuclease enzymes prior to being translated.

20 Alternatively, the expression of an endogenous gene in a cell, tissue or organ may be suppressed when one or more copies of said gene, or one or more copies of a substantially similar gene are introduced into the cell. Whilst the mechanism involved in this phenomenon has not been established and appears to be involve mechanistically heterogeneous processes. For example, this approach has been 25 postulated to involve transcriptional repression, in which case somatically-heritable repressed states of chromatin are formed or alternatively, a post-transcriptional silencing wherein transcription initiation occurs normally but the RNA products of the co-suppressed genes are subsequently eliminated.

30 The efficiency of both of these approaches in targeting the expression of specific

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genes is very low and highly variable results are usually obtained. Inconsistent results are obtained using different regions of genes, for example 5'- untranslated regions, 3'-untranslated regions, coding regions or intron sequences to target gene expression. Accordingly, there currently exists no consensus as to the nature of genetic sequences 5 which provide the most efficient means for repressing, delaying or otherwise reducing gene expression using existing technologies. Moreover, such a high degree of variation exists between generations such that it is not possible to predict the level of repression of a specific gene in the progeny of an organism in which gene expression was markedly modified.

10

Recently, Dorer and Henikoff (1994) demonstrated the silencing of tandemly repeated gene copies in the *Drosophila* genome and the transcriptional repression of dispersed *Drosophila Adh* genes by *Polycomb* genes (i.e. the *Pc-G* system; Pal-Bhadra et al, 1997). However, such silencing of tandemly repeated gene copies is of little utility in 15 an attempt to manipulate gene expression in an animal cell by recombinant means, wherein the sequences capable of targeting the expression of a particular gene are introduced at dispersed locations in the genome, absent the combination of this approach with gene-targeting technology. Whilst theoretically possible, such combinations would be expected to work at only low-efficiency, based upon the low 20 efficiency of gene-targeting approaches used in isolation and further, would require complicated vector systems. Additionally, the utilisation of transcriptional repression, such as the *Drosophila Pc-G* system, would appear to require some knowledge of the regulatory mechanisms capable of modulating the expression of any specific target gene and, as a consequence, would be difficult to implement in practice as a general 25 technology for repressing, delaying or reducing gene expression in animal cells.

The poor understanding of the mechanisms involved in these phenomena has meant that there have been few improvements in technologies for modulating the level of gene expression , in particular technologies for delaying, repressing or otherwise 30 reducing the expression of specific genes using recombinant DNA technology.

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Furthermore, as a consequence of the unpredictability of these approaches, there is currently no commercially-viable means for modulating the level of expression of a specific gene in a eukaryotic or prokaryotic organism.

- 5 Thus, there exists a need for improved methods of modulating gene expression, in particular repressing, delaying or otherwise reducing gene expression in animal cells for the purpose of introducing novel phenotypic traits thereto. In particular, these methods should provide general means for phenotypic modification, without the necessity for performing concomitant gene-targeting approaches.

10

#### SUMMARY OF THE INVENTION

The invention is based in part on the surprising discovery by the inventors that cells which exhibit one or more desired traits can be produced and selected from transformed cells comprising a nucleic acid molecule operably linked to a promoter, 15 wherein the transcription product of the nucleic acid molecule comprises a nucleotide sequence which is substantially identical to the nucleotide sequence of a transcript of an endogenous or non-endogenous target gene, the expression of which is intended to be modulated. The transformed cells are regenerated into whole tissues, organs or organisms capable of exhibiting novel traits, in particular virus resistance and 20 modified expression of endogenous genes.

Accordingly, one aspect of the present invention provides a method of modulating the expression of a target gene in an animal cell, tissue or organ, said method at least comprising the step of introducing to said cell, tissue or organ one or more dispersed 25 nucleic acid molecules or foreign nucleic acid molecules comprising multiple copies of a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a region thereof or complementary thereto for a time and under conditions sufficient for translation of the mRNA product of said target gene to be modified, subject to the proviso that the transcription of said mRNA product is not 30 exclusively repressed or reduced.

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In a particularly preferred embodiment, the dispersed nucleic acid molecules or foreign nucleic acid molecules comprises a nucleotide sequence which encodes multiple copies of an mRNA molecule which is substantially identical to the nucleotide sequence of the mRNA product of the target gene. More preferably, the multiple copies 5 of the target molecule are tandem direct repeat sequences.

In a more particularly preferred embodiment, the dispersed nucleic acid molecule or foreign nucleic acid molecule is in an expressible form such that it is at least capable of being transcribed to produce mRNA.

10

The target gene may be a gene which is endogenous to the animal cell or alternatively, a foreign gene such as a viral or foreign genetic sequence, amongst others. Preferably, the target gene is a viral genetic sequence.

15 The invention is particularly useful in the modulation of eukaryotic gene expression, in particular the modulation of human or animal gene expression and even more particularly in the modulation of expression of genes derived from vertebrate and invertebrate animals, such as insects, aquatic animals (eg. fish, shellfish, molluscs, crustaceans such as crabs, lobsters and prawns, avian animals and mammals, 20 amongst others).

A variety of traits are selectable with appropriate procedures and sufficient numbers of transformed cells. Such traits include, but are not limited to, visible traits, disease-resistance traits, and pathogen-resistance traits. The modulatory effect is applicable 25 to a variety of genes expressed in plants and animals including, for example, endogenous genes responsible for cellular metabolism or cellular transformation, including oncogenes, transcription factors and other genes which encode polypeptides involved in cellular metabolism.

30 For example, an alteration in the pigment production in mice can be engineered by

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targeting the expression of the tyrosinase gene therein. This provides a novel phenotype of albinism in black mice. By targeting genes required for virus replication in a plant cell or an animal cell, a genetic construct which comprises multiple copies of nucleotide sequence encoding a viral replicase, polymerase, coat protein or 5 uncoating gene, or protease protein, may be introduced into a cell where it is expressed, to confer immunity against the virus upon the cell.

In performance of the present invention, the dispersed nucleic acid molecule or foreign nucleic acid molecule will generally comprise a nucleotide sequence having greater 10 than about 85% identity to the target gene sequence, however, a higher homology might produce a more effective modulation of expression of the target gene sequence. Substantially greater homology, or more than about 90% is preferred, and even more preferably about 95% to absolute identity is desirable.

15 The introduced dispersed nucleic acid molecule or foreign nucleic acid molecule sequence, needing less than absolute homology, also need not be full length, relative to either the primary transcription product or fully processed mRNA of the target gene. A higher homology in a shorter than full length sequence compensates for a longer less homologous sequence. Furthermore, the introduced sequence need not have the 20 same intron or exon pattern, and homology of non-coding segments will be equally effective. Normally, a sequence of greater than 20-100 nucleotides should be used, though a sequence of greater than about 200-300 nucleotides would be preferred, and a sequence of greater than 500-1000 nucleotides would be especially preferred depending on the size of the target gene.

25

A second aspect of the present invention provides a synthetic gene which is capable of modifying target gene expression in a cell, tissue or organ of a prokaryotic or eukaryotic organism which is transfected or transformed therewith, wherein said synthetic gene at least comprises a dispersed nucleic acid molecular foreign nucleic 30 acid molecule comprising multiple copies of a nucleotide sequence which is

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substantially identical to the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto placed operably under the control of a promoter sequence which is operable in said cell, tissue or organ.

- 5 A third aspect of the invention provides a synthetic gene which is capable of modifying the expression of a target gene in a cell, tissue or organ of a prokaryotic or eukaryotic organism which is transfected or transformed therewith, wherein said synthetic gene at least comprises multiple structural gene sequences, wherein each of said structural gene sequences comprises a nucleotide sequence which is substantially identical to  
10 the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto and wherein said multiple structural gene sequences are placed operably under the control of a single promoter sequence which is operable in said cell, tissue or organ.
- 15 A fourth aspect of the present invention provides a synthetic gene which is capable of modifying the expression of a target gene in a cell, tissue or organ of a prokaryote or eukaryote which is transfected or transformed therewith wherein said synthetic gene at least comprises multiple structural gene sequences wherein each of said structural gene sequences is placed operably under the control of a promoter sequence which  
20 is operable in said cell, tissue or organ and wherein each of said structural gene sequences comprises a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto.
- 25 A fifth aspect of the present invention provides a genetic construct which is capable of modifying the expression of an endogenous gene or target gene in a transformed or transfected cell, tissue or organ wherein said genetic construct at least comprises the synthetic gene of the invention and one or more origins of replication and/or selectable marker gene sequences.

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TABLE 1

5 Amino Acid	Three-letter code	One-letter code
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Asparagine	Asn	N
10 Aspartic acid	Asp	D
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid	Glu	E
Glycine	Gly	G
15 Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
20 Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
25 Tyrosine	Tyr	Y
Valine	Val	V
Aspartate/Asparagine	Baa	B
Glutamate/Glutamine	Zaa	Z
Any amino acid	Xaa	X

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(54) Title: CONTROL OF GENE EXPRESSION			
(57) Abstract			
<p>The present invention relates generally to a method of modifying gene expression and to synthetic genes for modifying endogenous gene expression in a cell, tissue or organ of a transgenic organism, in particular a transgenic animal or plant. More particularly, the present invention utilises recombinant DNA technology to post-transcriptionally modify or modulate the expression of a target gene in a cell, tissue, organ or whole organism, thereby producing novel phenotypes. Novel synthetic genes and genetic constructs which are capable of repressing, delaying or otherwise reducing the expression of an endogenous gene or a target gene in an organism when introduced thereto are also provided.</p>			

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## CONTROL OF GENE EXPRESSION

### FIELD OF THE INVENTION

The present invention relates generally to a method of modifying gene expression and  
5 to synthetic genes for modifying endogenous gene expression in a cell, tissue or organ  
of a transgenic organism, in particular a transgenic animal or plant. More particularly,  
the present invention utilises recombinant DNA technology to post-transcriptionally  
modify or modulate the expression of a target gene in a cell, tissue, organ or whole  
organism, thereby producing novel phenotypes. Novel synthetic genes and genetic  
10 constructs which are capable of repressing delaying or otherwise reducing the  
expression of an endogenous gene or a target gene in an organism when introduced  
thereto are also provided.

### GENERAL

15 Bibliographic details of the publications referred to in this specification are collected at  
the end of the description.

As used herein the term "derived from" shall be taken to indicate that a specified  
integer may be obtained from a particular specified source or species, albeit not  
20 necessarily directly from that specified source or species.

Throughout this specification, unless the context requires otherwise, the word  
"comprise", or variations such as "comprises" or "comprising", will be understood to  
imply the inclusion of a stated step or element or integer or group of steps or elements  
25 or integers but not the exclusion of any other step or element or integer or group of  
elements or integers.

Those skilled in the art will appreciate that the invention described herein is susceptible  
to variations and modifications other than those specifically described. It is to be  
30 understood that the invention includes all such variations and modifications. The

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invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations or any two or more of said steps or features.

- 5 The present invention is not to be limited in scope by the specific embodiments described herein, which are intended for the purposes of exemplification only. Functionally-equivalent products, compositions and methods are clearly within the scope of the invention, as described herein.
- 10 Sequence identity numbers (SEQ ID.NOS.) containing nucleotide and amino acid sequence information included in this specification are collected after the Abstract and have been prepared using the programme PatentIn Version 2.0. Each nucleotide or amino acid sequence is identified in the sequence listing by the numeric indicator <210> followed by the sequence identifier (e.g. <210>1, <210>2, etc). The length, type  
15 of sequence (DNA, protein (PRT), etc) and source organism for each nucleotide or amino acid sequence are indicated by information provided in the numeric indicator fields <211>, <212> and <213>, respectively. Nucleotide and amino acid sequences referred to in the specification are defined by the information provided in numeric indicator field <400> followed by the sequence identifier (eg. <400>1, <400>2, etc).

20

The designation of nucleotide residues referred to herein are those recommended by the IUPAC-IUB Biochemical Nomenclature Commission, wherein A represents Adenine, C represents Cytosine, G represents Guanine, T represents thymine, Y represents a pyrimidine residue, R represents a purine residue, M represents Adenine  
25 or Cytosine, K represents Guanine or Thymine, S represents Guanine or Cytosine, W represents Adenine or Thymine, H represents a nucleotide other than Guanine, B represents a nucleotide other than Adenine; V represents a nucleotide other than Thymine, D represents a nucleotide other than Cytosine and N represents any nucleotide residue.

30

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The designation of amino acid residues referred to herein, as recommended by the IUPAC-IUB Biochemical Nomenclature Commission, are listed in Table 1.

**TABLE 1**

5 Amino Acid	Three-letter code	One-letter code
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
10 Aspartic acid	Asp	D
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid	Glu	E
Glycine	Gly	G
15 Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
20 Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
25 Tyrosine	Tyr	Y
Valine	Val	V
Aspartate/Asparagine	Baa	B
Glutamate/Glutamine	Zaa	Z
Any amino acid	Xaa	X

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## BACKGROUND TO THE INVENTION

Controlling metabolic pathways in eukaryotic organisms is desirable for the purposes of producing novel traits therein or introducing novel traits into a particular cell, tissue or organ of said organism. Whilst recombinant DNA technology has provided 5 significant progress in an understanding of the mechanisms regulating eukaryotic gene expression, much less progress has been made in the actual manipulation of gene expression to produce novel traits. Moreover, there are only limited means by which human intervention may lead to a modulation of the level of eukaryotic gene expression.

10

One approach to repressing, delaying or otherwise reducing gene expression utilise a mRNA molecule which is transcribed from the complementary strand of a nuclear gene to that which is normally transcribed and capable of being translated into a polypeptide. Although the precise mechanism involved in this approach is not 15 established, it has been postulated that a double-stranded mRNA may form by base pairing between the complementary nucleotide sequences, to produce a complex which is translated at low efficiency and/or degraded by intracellular ribonuclease enzymes prior to being translated.

- 20 Alternatively, the expression of an endogenous gene in a cell, tissue or organ may be suppressed when one or more copies of said gene, or one or more copies of a substantially similar gene are introduced into the cell. Whilst the mechanism involved in this phenomenon has not been established and appears to be involve mechanistically heterogeneous processes. For example, this approach has been 25 postulated to involve transcriptional repression, in which case somatically-heritable repressed states of chromatin are formed or alternatively, a post-transcriptional silencing wherein transcription initiation occurs normally but the RNA products of the co-suppressed genes are subsequently eliminated.
- 30 The efficiency of both of these approaches in targeting the expression of specific

genes is very low and highly variable results are usually obtained. Inconsistent results are obtained using different regions of genes, for example 5'- untranslated regions, 3'-untranslated regions, coding regions or intron sequences to target gene expression. Accordingly, there currently exists no consensus as to the nature of genetic sequences 5 which provide the most efficient means for repressing, delaying or otherwise reducing gene expression using existing technologies. Moreover, such a high degree of variation exists between generations such that it is not possible to predict the level of repression of a specific gene in the progeny of an organism in which gene expression was markedly modified.

10

Recently, Dorer and Henikoff (1994) demonstrated the silencing of tandemly repeated gene copies in the *Drosophila* genome and the transcriptional repression of dispersed *Drosophila Adh* genes by *Polycomb* genes (i.e. the *Pc-G* system; Pal-Bhadra *et al*, 1997). However, such silencing of tandemly repeated gene copies is of little utility in 15 an attempt to manipulate gene expression in an animal cell by recombinant means, wherein the sequences capable of targeting the expression of a particular gene are introduced at dispersed locations in the genome, absent the combination of this approach with gene-targeting technology. Whilst theoretically possible, such combinations would be expected to work at only low-efficiency, based upon the low 20 efficiency of gene-targeting approaches used in isolation and further, would require complicated vector systems. Additionally, the utilisation of transcriptional repression, such as the *Drosophila Pc-G* system, would appear to require some knowledge of the regulatory mechanisms capable of modulating the expression of any specific target gene and, as a consequence, would be difficult to implement in practice as a general 25 technology for repressing, delaying or reducing gene expression in animal cells.

The poor understanding of the mechanisms involved in these phenomena has meant that there have been few improvements in technologies for modulating the level of gene expression , in particular technologies for delaying, repressing or otherwise 30 reducing the expression of specific genes using recombinant DNA technology.

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Furthermore, as a consequence of the unpredictability of these approaches, there is currently no commercially-viable means for modulating the level of expression of a specific gene in a eukaryotic or prokaryotic organism.

- 5 Thus, there exists a need for improved methods of modulating gene expression, in particular repressing, delaying or otherwise reducing gene expression in animal cells for the purpose of introducing novel phenotypic traits thereto. In particular, these methods should provide general means for phenotypic modification, without the necessity for performing concomitant gene-targeting approaches.

10

#### **SUMMARY OF THE INVENTION**

The invention is based in part on the surprising discovery by the inventors that cells which exhibit one or more desired traits can be produced and selected from transformed cells comprising a nucleic acid molecule operably linked to a promoter, 15 wherein the transcription product of the nucleic acid molecule comprises a nucleotide sequence which is substantially identical to the nucleotide sequence of a transcript of an endogenous or non-endogenous target gene, the expression of which is intended to be modulated. The transformed cells are regenerated into whole tissues, organs or organisms capable of exhibiting novel traits, in particular virus resistance and 20 modified expression of endogenous genes.

Accordingly, one aspect of the present invention provides a method of modulating the expression of a target gene in an animal cell, tissue or organ, said method at least comprising the step of introducing to said cell, tissue or organ one or more dispersed 25 nucleic acid molecules or foreign nucleic acid molecules comprising multiple copies of a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a region thereof or complementary thereto for a time and under conditions sufficient for translation of the mRNA product of said target gene to be modified, subject to the proviso that the transcription of said mRNA product is not 30 exclusively repressed or reduced.

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In a particularly preferred embodiment, the dispersed nucleic acid molecules or foreign nucleic acid molecules comprises a nucleotide sequence which encodes multiple copies of an mRNA molecule which is substantially identical to the nucleotide sequence of the mRNA product of the target gene. More preferably, the multiple copies 5 of the target molecule are tandem direct repeat sequences.

In a more particularly preferred embodiment, the dispersed nucleic acid molecule or foreign nucleic acid molecule is in an expressible form such that it is at least capable of being transcribed to produce mRNA.

10

The target gene may be a gene which is endogenous to the animal cell or alternatively, a foreign gene such as a viral or foreign genetic sequence, amongst others. Preferably, the target gene is a viral genetic sequence.

15 The invention is particularly useful in the modulation of eukaryotic gene expression, in particular the modulation of human or animal gene expression and even more particularly in the modulation of expression of genes derived from vertebrate and invertebrate animals, such as insects, aquatic animals (eg. fish, shellfish, molluscs, crustaceans such as crabs, lobsters and prawns, avian animals and mammals, 20 amongst others).

A variety of traits are selectable with appropriate procedures and sufficient numbers of transformed cells. Such traits include, but are not limited to, visible traits, disease-resistance traits, and pathogen-resistance traits. The modulatory effect is applicable 25 to a variety of genes expressed in plants and animals including, for example, endogenous genes responsible for cellular metabolism or cellular transformation, including oncogenes, transcription factors and other genes which encode polypeptides involved in cellular metabolism.

30 For example, an alteration in the pigment production in mice can be engineered by

targeting the expression of the tyrosinase gene therein. This provides a novel phenotype of albinism in black mice. By targeting genes required for virus replication in a plant cell or an animal cell, a genetic construct which comprises multiple copies of nucleotide sequence encoding a viral replicase, polymerase, coat protein or 5 uncoating gene, or protease protein, may be introduced into a cell where it is expressed, to confer immunity against the virus upon the cell.

In performance of the present invention, the dispersed nucleic acid molecule or foreign nucleic acid molecule will generally comprise a nucleotide sequence having greater 10 than about 85% identity to the target gene sequence, however, a higher homology might produce a more effective modulation of expression of the target gene sequence. Substantially greater homology, or more than about 90% is preferred, and even more preferably about 95% to absolute identity is desirable.

15 The introduced dispersed nucleic acid molecule or foreign nucleic acid molecule sequence, needing less than absolute homology, also need not be full length, relative to either the primary transcription product or fully processed mRNA of the target gene. A higher homology in a shorter than full length sequence compensates for a longer less homologous sequence. Furthermore, the introduced sequence need not have the 20 same intron or exon pattern, and homology of non-coding segments will be equally effective. Normally, a sequence of greater than 20-100 nucleotides should be used, though a sequence of greater than about 200-300 nucleotides would be preferred, and a sequence of greater than 500-1000 nucleotides would be especially preferred depending on the size of the target gene.

25

A second aspect of the present invention provides a synthetic gene which is capable of modifying target gene expression in a cell, tissue or organ of a prokaryotic or eukaryotic organism which is transfected or transformed therewith, wherein said synthetic gene at least comprises a dispersed nucleic acid molecular foreign nucleic 30 acid molecule comprising multiple copies of a nucleotide sequence which is

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substantially identical to the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto placed operably under the control of a promoter sequence which is operable in said cell, tissue or organ.

- 5 A third aspect of the invention provides a synthetic gene which is capable of modifying the expression of a target gene in a cell, tissue or organ of a prokaryotic or eukaryotic organism which is transfected or transformed therewith, wherein said synthetic gene at least comprises multiple structural gene sequences, wherein each of said structural gene sequences comprises a nucleotide sequence which is substantially identical to  
10 the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto and wherein said multiple structural gene sequences are placed operably under the control of a single promoter sequence which is operable in said cell, tissue or organ.
- 15 A fourth aspect of the present invention provides a synthetic gene which is capable of modifying the expression of a target gene in a cell, tissue or organ of a prokaryote or eukaryote which is transfected or transformed therewith wherein said synthetic gene at least comprises multiple structural gene sequences wherein each of said structural gene sequences is placed operably under the control of a promoter sequence which  
20 is operable in said cell, tissue or organ and wherein each of said structural gene sequences comprises a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto.
- 25 A fifth aspect of the present invention provides a genetic construct which is capable of modifying the expression of an endogenous gene or target gene in a transformed or transfected cell, tissue or organ wherein said genetic construct at least comprises the synthetic gene of the invention and one or more origins of replication and/or selectable marker gene sequences.

- 10 -

In order to observe many novel traits in multicellular organisms such as plants and animals, in particular those which are tissue-specific or organ-specific or developmentally-regulated, regeneration of a transformed cell carrying the synthetic genes and genetic constructs described herein into a whole organism will be required.

- 5 Those skilled in the art will be aware that this means growing a whole organism from a transformed plant cell or animal cell, a group of such cells, a tissue or organ. Standard methods for the regeneration of certain plants and animals from isolated cells and tissues are known to those skilled in the art.
- 10 Accordingly, a sixth aspect of the invention provides a cell, tissue, organ or organism comprising the synthetic genes and genetic constructs described herein.

#### BRIEF DESCRIPTION OF THE DRAWINGS

- 15 **Figure 1** is a diagrammatic representation of the plasmid pEGFP-N1 MCS.

**Figure 2** is a diagrammatic representation of the plasmid pCMV.cass.

**Figure 3** is a diagrammatic representation of the plasmid pCMV.SV40L.cass.

20

**Figure 4** is a diagrammatic representation of the plasmid pCMV.SV40LR.cass.

**Figure 5** is a diagrammatic representation of the plasmid pCR.Bgl-GFP-Bam.

- 25 **Figure 6** is a diagrammatic representation of the plasmid pBSII(SK+).EGFP.

**Figure 7** is a diagrammatic representation of the plasmid pCMV.EGFP.

**Figure 8** is a diagrammatic representation of the plasmid pCR.SV40L.

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**Figure 9** is a diagrammatic representation of the plasmid pCR.BEV.1.

**Figure 10** is a diagrammatic representation of the plasmid pCR.BEV.2.

5 **Figure 11** is a diagrammatic representation of the plasmid pCR.BEV.3.

**Figure 12** is a diagrammatic representation of the plasmid pCMV.EGFP.BEV2.

**Figure 13** is a diagrammatic representation of the plasmid pCMV.BEV.2.

10

**Figure 14** is a diagrammatic representation of the plasmid pCMV.BEV.3.

**Figure 15** is a diagrammatic representation of the plasmid pCMV.VEB.

15 **Figure 16** is a diagrammatic representation of the plasmid pCMV.BEV.GFP.

**Figure 17** is a diagrammatic representation of the plasmid pCMV.BEV.SV40L-0.

**Figure 18** is a diagrammatic representation of the plasmid pCMV.0.SV40L.BEV.

20

**Figure 19** is a diagrammatic representation of the plasmid pCMV.0.SV40L.VEB.

**Figure 20** is a diagrammatic representation of the plasmid pCMV.BEVx2.

25 **Figure 21** is a diagrammatic representation of the plasmid pCMV.BEVx3.

**Figure 22** is a diagrammatic representation of the plasmid pCMV.BEVx4.

**Figure 23** is a diagrammatic representation of the plasmid pCMV.BEV.SV40L.BEV.

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**Figure 24** is a diagrammatic representation of the plasmid pCMV.BEV.SV40L.VEB.

**Figure 25** is a diagrammatic representation of the plasmid pCMV.BEV.GFP.VEB.

5 **Figure 26** is a diagrammatic representation of the plasmid pCMV.EGFP.BEV2.PFG.

**Figure 27** is a diagrammatic representation of the plasmid pCMV.BEV.SV40LR.

**Figure 28** is a diagrammatic representation of the plasmid pCDNA3.Galt.

10

**Figure 29** is a diagrammatic representation of the plasmid pCMV.Galt.

**Figure 30** is a diagrammatic representation of the plasmid pCMV.EGFP.Galt.

15 **Figure 31** is a diagrammatic representation of the plasmid pCMV.Galt.GFP.

**Figure 32** is a diagrammatic representation of the plasmid pCMV.Galt.SV40L.O.

**Figure 33** is a diagrammatic representation of the plasmid pCMV.Galt.SV40L.tlaG.

20

**Figure 34** is a diagrammatic representation of the plasmid pCMV.O.SV40L.Galt.

**Figure 35** is a diagrammatic representation of the plasmid pCMV.Galtx2.

25 **Figure 36** is a diagrammatic representation of the plasmid pCMV.Galtx4.

**Figure 37** is a diagrammatic representation of the plasmid pCMV.Galt.SV40L.Galt.

**Figure 38** is a diagrammatic representation of the plasmid pCMV.Galt.SV40L.tlaG.

30

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**Figure 39** is a diagrammatic representation of the plasmid pCMV.Galt.GFP.tlaG.

**Figure 40** is a diagrammatic representation of the plasmid pCMV.EGFP.Galt.PFG.

5 **Figure 41** is a diagrammatic representation of the plasmid pCMV.Galt.SV40LR.

**Figure 42** is a diagrammatic representation of the plasmid pART7.

**Figure 43** is a diagrammatic representation of the plasmid pART7.35S.SCBV.cass.

10

**Figure 44** is a diagrammatic representation of the plasmid pBC.PVY.

**Figure 45** is a diagrammatic representation of the plasmid pSP72.PVY.

15 **Figure 46** is a diagrammatic representation of the plasmid pClapBC.PVY.

**Figure 47** is a diagrammatic representation of the plasmid pBC.PVYx2.

**Figure 48** is a diagrammatic representation of the plasmid pSP72.PVYx2.

20

**Figure 49** is a diagrammatic representation of the plasmid pBC.PVYx3.

**Figure 50** is a diagrammatic representation of the plasmid pBC.PVYx4.

25 **Figure 51** is a diagrammatic representation of the plasmid pBC.PVY.LNYV.

**Figure 52** is a diagrammatic representation of the plasmid pBC.PVY.LNYV.PVY.

**Figure 53** is a diagrammatic representation of the plasmid pBC.PVY.LNYV.YVP<sub>Δ</sub>.

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**Figure 54** is a diagrammatic representation of the plasmid pBC.PVY.LNYV.YVP.

**Figure 55** is a diagrammatic representation of the plasmid pART27.PVY

5 **Figure 56** is a diagrammatic representation of the plasmid pART27.35S.PVY.SCBV.O.

**Figure 57** is a diagrammatic representation of the plasmid pART27.35S.O.SCBV.PVY.

**Figure 58** is a diagrammatic representation of the plasmid pART27.35S.O.SCBV.YVP.

10

**Figure 59** is a diagrammatic representation of the plasmid pART7.PVYx2.

**Figure 60** is a diagrammatic representation of the plasmid pART7.PVYx3.

15 **Figure 61** is a diagrammatic representation of the plasmid pART7.PVYx4.

**Figure 62** is a diagrammatic representation of the plasmid pART7.PVY.LNYV.PVY.

**Figure 63** is a diagrammatic representation of the plasmid pART7.PVY.LNYV.YVP<sub>A</sub>.

20

**Figure 64** is a diagrammatic representation of the plasmid pART7.PVY.LNYV.YVP.

**Figure 65** is a diagrammatic representation of pART7.35S.PVY.SCBV.YVP.

25 **Figure 66** is a diagrammatic representation of pART7.35S.PVYx3.SCBV.YVPx3.

**Figure 67** is a diagrammatic representation of pART7.PVYx3.LNYV.YVPx3.

**Figure 68** is a diagrammatic representation of the plasmid pART7.PVYMULTI.

30

**DETAILED DESCRIPTION OF THE INVENTION**

The present invention provides a method of modulating the expression of a target gene in a cell, tissue or organ, said method at least comprising the step of introducing to 5 said cell, tissue or organ one or more dispersed nucleic acid molecules or foreign nucleic acid molecules comprising multiple copies of a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a region thereof or complementary thereto for a time and under conditions sufficient for translation of the mRNA product of said target gene to be modified, subject to the 10 proviso that the transcription of said mRNA product is not exclusively repressed or reduced.

By "multiple copies" is meant that two or more copies of the target gene are presented in close physical connection or juxtaposed, in the same or different orientation, on the 15 same nucleic acid molecule, optionally separated by a stuffer fragment or intergenic region to facilitate secondary structure formation between each repeat where this is required. The stuffer fragment may comprise any combination of nucleotide or amino acid residues, carbohydrate molecules or oligosaccharide molecules or carbon atoms or a homologue, analogue or derivative thereof which is capable of being linked 20 covalently to a nucleic acid molecule.

Preferably, embodiment, the stuffer fragment comprises a sequence of nucleotides or a homologue, analogue or derivative thereof.

- 25 More preferably, the stuffer fragment comprises a sequence of nucleotides of at least about 10-50 nucleotides in length, even more preferably at least about 50-100 nucleotides in length and still more preferably at least about 100-500 nucleotides in length.
- 30 Wherein the dispersed or foreign nucleic acid molecule comprises intron/exon splice

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junction sequences, the stuffer fragment may serve as an intron sequence placed between the 3'-splice site of the structural gene nearer the 5'-end of the gene and the 5'- splice site of the next downstream unit thereof. Alternatively, wherein it is desirable for more than two adjacent nucleotide sequence units of the dispersed foreign nucleic acid molecule to be translated, the stuffer fragment placed there between should not include an in-frame translation stop codon, absent intron/exon splice junction sequences at both ends of the stuffer fragment or the addition of a translation start codon at the 5' end of each unit, as will be obvious to those skilled in the art.

- 5 10 Preferred stuffer fragments are those which encode detectable marker proteins or biologically-active analogues and derivatives thereof, for example luciferase,  $\beta$ -galacturonase,  $\beta$ -galactosidase, chloramphenicol acetyltransferase or green fluorescent protein, amongst others. Additional stuffer fragments are not excluded.
- 15 According to this embodiment, the detectable marker or an analogue or derivative thereof serves to indicate the expression of the synthetic gene of the invention in a cell, tissue or organ by virtue of its ability to confer a specific detectable phenotype thereon, preferably a visually-detectable phenotype.
- 20 As used herein, the term "modulating" shall be taken to mean that expression of the target gene is reduced in amplitude and/or the timing of gene expression is delayed and/or the developmental or tissue-specific or cell-specific pattern of target gene expression is altered, compared to the expression of said gene in the absence of the inventive method described herein.

25

Whilst not limiting the scope of the invention described herein, the present invention is directed to a modulation of gene expression which comprises the repression, delay or reduction in amplitude of target gene expression in a specified cell, tissue or organ of a eukaryotic organism, in particular a plant such as a monocotyledonous or 30 dicotyledonous plant, or a human or other animal and even more particularly a

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vertebrate and invertebrate animal, such as an insect, aquatic animal (eg. fish, shellfish, mollusc, crustacean such as a crab, lobster or prawn, an avian animal or a mammal, amongst others).

- 5 More preferably, target gene expression is completely inactivated by the dispersed nucleic acid molecules or foreign nucleic acid molecules which has been introduced to the cell, tissue or organ.

Whilst not being bound by any theory or mode of action, the reduced or eliminated  
10 expression of the target gene which results from the performance of the invention may be attributed to reduced or delayed translation of the mRNA transcription product of the target gene or alternatively, the prevention of translation of said mRNA, as a consequence of sequence-specific degradation of the mRNA transcript of the target gene by an endogenous host cell system.

15

It is particularly preferred that, for optimum results, sequence-specific degradation of the mRNA transcript of the target gene occurs either prior to the time or stage when the mRNA transcript of the target gene would normally be translated or alternatively, at the same time as the mRNA transcript of the target gene would normally be  
20 translated. Accordingly, the selection of an appropriate promoter sequence to regulate expression of the introduced dispersed nucleic acid molecule or foreign nucleic acid molecule is an important consideration to optimum performance of the invention. For this reason, strong constitutive promoters or inducible promoter systems are especially preferred for use in regulating expression of the introduced dispersed nucleic acid  
25 molecules or foreign nucleic acid molecules.

The present invention clearly encompasses reduced expression wherein reduced expression of the target gene is effected by lowered transcription, subject to the proviso that a reduction in transcription is not the sole mechanism by which this occurs  
30 and said reduction in transcription is at least accompanied by reduced translation of

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the steady-state mRNA pool.

The target gene may be a genetic sequence which is endogenous to the animal cell or alternatively, a non-endogenous genetic sequence, such as a genetic sequence 5 which is derived from a virus or other foreign pathogenic organism and is capable of entering a cell and using the cell's machinery following infection.

Wherein the target gene is a non-endogenous genetic sequence to the animal cell, it is desirable that the target gene encodes a function which is essential for replication 10 or reproduction of the viral or other pathogen. In such embodiments, the present invention is particularly useful in the prophylactic and therapeutic treatment of viral infection of an animal cell or for conferring or stimulating resistance against said pathogen.

15 Preferably, the target gene comprises one or more nucleotide sequences of a viral pathogen of a plant or an animal cell, tissue or organ.

For example, in the case of animals and humans, the viral pathogen may be a retrovirus, for example a lentivirus such as the immunodeficiency viruses, a single-20 stranded (+) RNA virus such as bovine enterovirus (BEV) or Sinbis alphavirus. Alternatively, the target gene can comprise one or more nucleotide sequences of a viral pathogen of an animal cell, tissue or organ, such as but not limited to a double-stranded DNA virus such as bovine herpes virus or herpes simplex virus I (HSV I), amongst others.

25

In the case of plants, the virus pathogen is preferably a potyvirus, caulimovirus, badnavirus, geminivirus, reovirus, rhabdovirus, bunyavirus, tospovirus, tenuivirus, tombusvirus, luteovirus, sobemovirus, bromovirus, cucomovirus, ilavivirus, alfamovirus, tobamovirus, tobaviruses, potexvirus and clostrovirus, such as but not limited to CaMV, 30 SCSV, PVX, PVY, PLRV, and TMV, amongst others.

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With particular regard to viral pathogens, those skilled in the art are aware that virus-encoded functions may be complemented *in trans* by polypeptides encoded by the host cell. For example, the replication of the bovine herpes virus genome in the host cell may be facilitated by host cell DNA polymerases which are capable of 5 complementing an inactivated viral DNA polymerase gene.

Accordingly, wherein the target gene is a non-endogenous genetic sequence to the animal cell, a further alternative embodiment of the invention provides for the target gene to encode a viral or foreign polypeptide which is not capable of being 10 complemented by a host cell function, such as a virus-specific genetic sequence. Exemplary target genes according to this embodiment of the invention include, but are not limited to genes which encode virus coat proteins, uncoating proteins and RNA-dependent DNA polymerases and RNA-dependent RNA polymerases, amongst others.

15 In a particularly preferred embodiment of the present invention, the target gene is the BEV RNA-dependent RNA polymerase gene or a homologue, analogue or derivative thereof or PVY Nia protease-encoding sequences.

The cell in which expression of the target gene is modified may be any cell which is 20 derived from a multicellular plant or animal, including cell and tissue cultures thereof. Preferably, the animal cell is derived from an insect, reptile, amphibian, bird, human or other mammal. Exemplary animal cells include embryonic stem cells, cultured skin fibroblasts, neuronal cells, somatic cells, haematopoietic stem cells, T-cells and immortalised cell lines such as COS, VERO, HeLa, mouse C127, Chinese hamster 25 ovary (CHO), WI-38, baby hamster kidney (BHK) or MDBK cell lines, amongst others. Such cells and cell lines are readily available to those skilled in the art. Accordingly, the tissue or organ in which expression of the target gene is modified may be any tissue or organ comprising such animal cells.

30 Preferably the plant cell is derived from a monocotyledonous or dicotyledonous plant

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species or a cell line derived therefrom.

As used herein, the term "dispersed nucleic acid molecule" shall be taken to refer to a nucleic acid molecule which comprises one or more multiple copies, preferably 5 tandem direct repeats, of a nucleotide sequence which is substantially identical or complementary to the nucleotide sequence of a gene which originates from the cell, tissue or organ into which said nucleic acid molecule is introduced, wherein said nucleic acid molecule is non-endogenous in the sense that it is introduced to the cell, tissue or organ of an animal via recombinant means and will generally be present as 10 extrachromosomal nucleic acid or alternatively, as integrated chromosomal nucleic acid which is genetically-unlinked to said gene. More particularly, the "dispersed nucleic acid molecule" will comprise chromosomal or extrachromosomal nucleic acid which is unlinked to the target gene against which it is directed in a physical map, by virtue of their not being tandemly-linked or alternatively, occupying a different 15 chromosomal position on the same chromosome or being localised on a different chromosome or present in the cell as an episome, plasmid, cosmid or virus particle.

By "foreign nucleic acid molecule" is meant an isolated nucleic acid molecule which has one or more multiple copies, preferably tandem direct repeats, of a nucleotide 20 sequence which originates from the genetic sequence of an organism which is different from the organism to which the foreign nucleic acid molecule is introduced. This definition encompasses a nucleic acid molecule which originates from a different individual of the same lowest taxonomic grouping (i.e. the same population) as the taxonomic grouping to which said nucleic acid molecule is introduced, as well as a 25 nucleic acid molecule which originates from a different individual of a different taxonomic grouping as the taxonomic grouping to which said nucleic acid molecule is introduced, such as a gene derived from a viral pathogen.

Accordingly, a target gene against which a foreign nucleic acid molecule acts in the 30 performance of the invention may be a nucleic acid molecule which has been

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introduced from one organism to another organism using transformation or introgression technologies. Exemplary target genes according to this embodiment of the invention include the green fluorescent protein-encoding gene derived from the jellyfish *Aequoria victoria* (Prasher et al., 1992; International Patent Publication No. WO 5 95/07463), tyrosinase genes and in particular the murine tyrosinase gene (Kwon et al., 1988), the *Escherichia coli lacI* gene which is capable of encoding a polypeptide repressor of the *lacZ* gene, the porcine  $\alpha$ -1,3-galactosyltransferase gene (NCBI Accession No. L36535) exemplified herein, and the PVY and BEV structural genes exemplified herein or a homologue, analogue or derivative of said genes or a 10 complementary nucleotide sequence thereto.

The present invention is further useful for simultaneously targeting the expression of several target genes which are co-expressed in a particular cell, for example by using a dispersed nucleic acid molecule or foreign nucleic acid molecule which comprises 15 nucleotide sequences which are substantially identical to each of said co-expressed target genes.

By "substantially identical" is meant that the introduced dispersed or foreign nucleic acid molecule of the invention and the target gene sequence are sufficiently identical 20 at the nucleotide sequence level to permit base-pairing there between under standard intracellular conditions.

Preferably, the nucleotide sequence of each repeat in the dispersed or foreign nucleic acid molecule of the invention and the nucleotide sequence of a part of the target gene 25 sequence are at least about 80-85% identical at the nucleotide sequence level, more preferably at least about 85-90% identical, even more preferably at least about 90-95% identical and still even more preferably at least about 95-99% or 100% identical at the nucleotide sequence level.

30 Notwithstanding that the present invention is not limited by the precise number of

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repeated sequences in the dispersed nucleic acid molecule or the foreign nucleic acid molecule of the invention, it is to be understood that the present invention requires at least two copies of the target gene sequence to be expressed in the cell.

5 Preferably, the multiple copies of the target gene sequence are presented in the dispersed nucleic acid molecule or the foreign nucleic acid molecule as tandem inverted repeat sequences and/or tandem direct repeat sequences. Such configurations are exemplified by the "test plasmids" described herein that comprise Galt, BEV or PVY gene regions.

10

Preferably, the dispersed or foreign nucleic acid molecule which is introduced to the cell, tissue or organ comprises RNA or DNA.

15 Preferably, the dispersed or foreign nucleic acid molecule further comprises a nucleotide sequence or is complementary to a nucleotide sequence which is capable of encoding an amino acid sequence encoded by the target gene. Even more preferably, the nucleic acid molecule includes one or more ATG or AUG translational start codons.

20 Standard methods may be used to introduce the dispersed nucleic acid molecule or foreign nucleic acid molecule into the cell, tissue or organ for the purposes of modulating the expression of the target gene. For example, the nucleic acid molecule may be introduced as naked DNA or RNA, optionally encapsulated in a liposome, in a virus particle as attenuated virus or associated with a virus coat or a transport protein  
25 or inert carrier such as gold or as a recombinant viral vector or bacterial vector or as a genetic construct, amongst others.

Administration means include injection and oral ingestion (e.g. in medicated food material), amongst others.

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The subject nucleic acid molecules may also be delivered by a live delivery system such as using a bacterial expression system optimised for their expression in bacteria which can be incorporated into gut flora. Alternatively, a viral expression system can be employed. In this regard, one form of viral expression is the administration of a live 5 vector generally by spray, feed or water where an infecting effective amount of the live vector (e.g. virus or bacterium) is provided to the animal. Another form of viral expression system is a non-replicating virus vector which is capable of infecting a cell but not replicating therein. The non-replicating viral vector provides a means of introducing to the human or animal subject genetic material for transient expression 10 therein. The mode of administering such a vector is the same as a live viral vector.

The carriers, excipients and/or diluents utilised in delivering the subject nucleic acid molecules to a host cell should be acceptable for human or veterinary applications. Such carriers, excipients and/or diluents are well-known to those skilled in the art. 15 Carriers and/or diluents suitable for veterinary use include any and all solvents, dispersion media, aqueous solutions, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like. Except insofar as any conventional media or agent is incompatible with the active ingredient, use thereof in the composition is contemplated. Supplementary active ingredients can also be 20 incorporated into the compositions.

In an alternative embodiment, the invention provides a method of modulating the expression of a target gene in a cell, tissue or organ, said method at least comprising the steps of:

- 25           (i)     selecting one or more dispersed nucleic acid molecules or foreign nucleic acid molecules which comprise multiple copies of a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a region thereof or which is complementary thereto; and  
             (ii)   introducing said dispersed nucleic acid molecules or foreign nucleic acid  
30           molecules to said cell, tissue or organ for a time and under conditions sufficient

for translation of the mRNA product of said target gene to be modified, subject to the proviso that the transcription of said mRNA product is not exclusively repressed or reduced.

- 5 To select appropriate nucleotide sequences for targeting expression of the target gene, several approaches may be employed. In one embodiment, multiple copies of specific regions of characterised genes may be cloned in operable connection with a suitable promoter and assayed for efficacy in reducing target gene expression. Alternatively, shotgun libraries comprising multiple copies of genetic sequences may be produced  
10 and assayed for their efficacy in reducing target gene expression. The advantage associated with the latter approach is that it is not necessary to have any prior knowledge of the significance of any particular target gene in specifying an undesirable phenotype in the cell. For example, shotgun libraries comprising virus sub-genomic fragments may be employed and tested directly for their ability to confer virus immunity  
15 on the animal host cell, without prior knowledge of the role which any virus genes play in pathogenesis of the host cell.

As used herein, the term "shotgun library" is a set of diverse nucleotide sequences wherein each member of said set is preferably contained within a suitable plasmid,  
20 cosmid, bacteriophage or virus vector molecule which is suitable for maintenance and/or replication in a cellular host. The term "shotgun library" includes a representative library, in which the extent of diversity between the nucleotide sequences is numerous such that all sequences in the genome of the organism from which said nucleotide sequences is derived are present in the "set" or alternatively, a  
25 limited library in which there is a lesser degree of diversity between said sequences. The term "shotgun library" further encompasses random nucleotide sequences, wherein the nucleotide sequence comprises viral or cellular genome fragments, amongst others obtained for example by shearing or partial digestion of genomic DNA using restriction endonucleases, amongst other approaches. A "shotgun library"  
30 further includes cells, virus particles and bacteriophage particles comprising the

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individual nucleotide sequences of the diverse set.

Preferred shotgun libraries according to this embodiment of the invention are "representative libraries", comprising a set of tandem repeated nucleotide sequences 5 derived from a viral pathogen of a plant or an animal.

In a particularly preferred embodiment of the invention, the shotgun library comprises cells, virus particles or bacteriophage particles comprising a diverse set of tandem-repeated nucleotide sequences which encode a diverse set of amino acid sequences, 10 wherein the member of said diverse set of nucleotide sequences are placed operably under the control of a promoter sequence which is capable of directing the expression of said tandem-repeated nucleotide sequence in the cell.

Accordingly, the nucleotide sequence of each unit in the tandem-repeated sequence 15 may comprise at least about 1 to 200 nucleotides in length. The use of larger fragments, particularly employing randomly sheared nucleic acid derived from viral, plant or animal genomes, is not excluded.

The introduced nucleic acid molecule is preferably in an expressible form.

20

By "expressible form" is meant that the subject nucleic acid molecule is presented in an arrangement such that it may be expressed in the cell, tissue, organ or whole organism, at least at the transcriptional level (i.e. it is expressed in the animal cell to yield at least an mRNA product which is optionally translatable or translated to produce 25 a recombinant peptide, oligopeptide or polypeptide molecule).

By way of exemplification, in order to obtain expression of the dispersed nucleic acid molecule or foreign nucleic acid molecule in the cell, tissue or organ of interest, a synthetic gene or a genetic construct comprising said synthetic gene is produced, 30 wherein said synthetic gene comprises a nucleotide sequence as described *supra* in

operable connection with a promoter sequence which is capable of regulating expression therein. Thus, the subject nucleic acid molecule will be operably connected to one or more regulatory elements sufficient for eukaryotic transcription to occur.

5 Accordingly, a further alternative embodiment of the invention provides a method of modulating the expression of a target gene in an animal cell, tissue or organ, said method at least comprising the steps of:

- (i) selecting one or more dispersed nucleic acid molecules or foreign nucleic acid molecules which comprise multiple copies, preferably tandem repeats, of a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a region thereof or which is complementary thereto;
- (ii) producing a synthetic gene comprising said dispersed nucleic acid molecules or foreign nucleic acid molecules;
- 10 (iii) introducing said synthetic gene to said cell, tissue or organ; and
- (iv) expressing said synthetic gene in said cell, tissue or organ for a time and under conditions sufficient for translation of the mRNA product of said target gene to be modified, subject to the proviso that the transcription of said mRNA product is not exclusively repressed or reduced.

20

Reference herein to a "gene" or "genes" is to be taken in its broadest context and includes:

- (i) a classical genomic gene consisting of transcriptional and/or translational regulatory sequences and/or a coding region and/or non-translated sequences (i.e. 25 introns, 5'- and 3'- untranslated sequences); and/or
  - (ii) mRNA or cDNA corresponding to the coding regions (i.e. exons) and 5'- and 3'- untranslated sequences of the gene; and/or
  - (iii) a structural region corresponding to the coding regions (i.e. exons) optionally further comprising untranslated sequences and/or a heterologous promoter sequence
- 30 which consists of transcriptional and/or translational regulatory regions capable of

conferring expression characteristics on said structural region.

The term "gene" is also used to describe synthetic or fusion molecules encoding all or part of a functional product, in particular a sense or antisense mRNA product or a 5 peptide, oligopeptide or polypeptide or a biologically-active protein.

The term "synthetic gene" refers to a non-naturally occurring gene as hereinbefore defined which preferably comprises at least one or more transcriptional and/or translational regulatory sequences operably linked to a structural gene sequence.

10

The term "structural gene" shall be taken to refer to a nucleotide sequence which is capable of being transmitted to produce mRNA and optionally, encodes a peptide, oligopeptide, polypeptide or biologically active protein molecule. Those skilled in the art will be aware that not all mRNA is capable of being translated into a peptide, 15 oligopeptide, polypeptide or protein, for example if the mRNA lacks a functional translation start signal or alternatively, if the mRNA is antisense mRNA. The present invention clearly encompasses synthetic genes comprising nucleotide sequences which are not capable of encoding peptides, oligopeptides, polypeptides or biologically-active proteins. In particular, the present inventors have found that such 20 synthetic genes may be advantageous in modifying target gene expression in cells, tissues or organs of a prokaryotic or eukaryotic organism.

The term "structural gene region" refers to that part of a synthetic gene which comprises a dispersed nucleic acid molecule or foreign nucleic acid molecule as 25 described herein which is expressed in a cell, tissue or organ under the control of a promoter sequence to which it is operably connected. A structural gene region may comprise one or more dispersed nucleic acid molecules and/or foreign nucleic acid molecules operably under the control of a single promoter sequence or multiple promoter sequences. Accordingly, the structural gene region of a synthetic gene may 30 comprise a nucleotide sequence which is capable of encoding an amino acid

- sequence or is complementary thereto. In this regard, a structural gene region which is used in the performance of the instant invention may also comprise a nucleotide sequence which encodes an amino acid sequence yet lacks a functional translation initiation codon and/or a functional translation stop codon and, as a consequence, 5 does not comprise a complete open reading frame. In the present context, the term "structural gene region" also extends to a non-coding nucleotide sequences, such as 5'- upstream or 3'-downstream sequences of a gene which would not normally be translated in a eukaryotic cell which expresses said gene.
- 10 Accordingly, in the context of the present invention, a structural gene region may also comprise a fusion between two or more open reading frames of the same or different genes. In such embodiments, the invention may be used to modulate the expression of one gene, by targeting different non-contiguous regions thereof or alternatively, to simultaneously modulate the expression of several different genes, including different 15 genes of a multigene family. In the case of a fusion nucleic acid molecule which is non-endogenous to the animal cell and in particular comprises two or more nucleotide sequences derived from a viral pathogen, the fusion may provide the added advantage of conferring simultaneous immunity or protection against several pathogens, by targeting the expression of genes in said several pathogens. Alternatively or in 20 addition, the fusion may provide more effective immunity against any pathogen by targeting the expression of more than one gene of that pathogen.

Particularly preferred structural gene regions according to this aspect of the invention are those which include at least one translatable open reading frame, more preferably 25 further including a translational start codon located at the 5'-end of said open reading frame, albeit not necessarily at the 5'-terminus of said structural gene region. In this regard, notwithstanding that the structural gene region may comprise at least one translatable open reading frame and/or AUG or ATG translational start codon, the inclusion of such sequences in no way suggests that the present invention requires 30 translation of the introduced nucleic acid molecule to occur in order to modulate the

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expression of the target gene. Whilst not being bound by any theory or mode of action, the inclusion of at least one translatable open reading frame and/or translational start codon in the subject nucleic acid molecule may serve to increase stability of the mRNA transcription product thereof, thereby improving the efficiency of the invention.

5

The optimum number of structural gene sequences which may be involved in the synthetic gene of the present invention will vary considerably, depending upon the length of each of said structural gene sequences, their orientation and degree of identity to each other. For example, those skilled in the art will be aware of the inherent instability of palindromic nucleotide sequences *in vivo* and the difficulties associated with constructing long synthetic genes comprising inverted repeated nucleotide sequences, because of the tendency for such sequences to recombine *in vivo*. Notwithstanding such difficulties, the optimum number of structural gene sequences to be included in the synthetic genes of the present invention may be determined empirically by those skilled in the art, without any undue experimentation and by following standard procedures such as the construction of the synthetic gene of the invention using recombinase-deficient cell lines, reducing the number of repeated sequences to a level which eliminates or minimises recombination events and by keeping the total length of the multiple structural gene sequence to an acceptable limit, preferably no more than 5-10kb, more preferably no more than 2-5kb and even more preferably no more than 0.5-2.0kb in length.

Wherein the structural gene region comprises more than one dispersed nucleic acid molecule or foreign nucleic acid molecule it shall be referred to herein as a "multiple structural gene region" or similar term. The present invention clearly extends to the use of multiple structural gene regions which preferably comprise a direct repeat sequence, inverted repeat sequence or interrupted palindrome sequence of a particular structural gene, dispersed nucleic acid molecule or foreign nucleic acid molecule, or a fragment thereof.

- 30 -

- Each dispersed or foreign nucleic acid molecule contained within the multiple structural gene unit of the subject synthetic gene may comprise a nucleotide sequence which is substantially identical to a different target gene in the same organism. Such an arrangement may be of particular utility when the synthetic gene is intended to provide
- 5 protection against a pathogen in a cell, tissue or organ, in particular a viral pathogen, by modifying the expression of viral target genes. For example, the multiple structural gene may comprise nucleotide sequences (i.e. two or more dispersed or foreign nucleic acid molecules) which are substantially identical to two or more target genes selected from the list comprising DNA polymerase, RNA polymerase, Nia protease,
- 10 and coat protein or other target gene which is essential for viral infectivity, replication or reproduction. However, it is preferred with this arrangement that the structural gene units are selected such that the target genes to which they are substantially identical are normally expressed at approximately the same time (or later) in an infected cell, tissue or organ as (than) the multiple structural gene of the subject synthetic gene is
- 15 expressed under control of the promoter sequence. This means that the promoter controlling expression of the multiple structural gene will usually be selected to confer expression in the cell, tissue or organ over the entire life cycle of the virus when the viral target genes are expressed at different stages of infection.
- 20 As with the individual sequence units of a dispersed or foreign nucleic acid molecule, the individual units of the multiple structural gene may be spatially connected in any orientation relative to each other, for example head-to-head, head-to-tail or tail-to-tail and all such configurations are within the scope of the invention.
- 25 For expression in eukaryotic cells, the synthetic gene generally comprises, in addition to the nucleic acid molecule of the invention, a promoter and optionally other regulatory sequences designed to facilitate expression of the dispersed nucleic acid molecule or foreign nucleic acid molecule.
- 30 Reference herein to a "promoter" is to be taken in its broadest context and includes the

transcriptional regulatory sequences of a classical genomic gene, including the TATA box which is required for accurate transcription initiation, with or without a CCAAT box sequence and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers) which alter gene expression in response to developmental 5 and/or external stimuli, or in a tissue-specific manner. A promoter is usually, but not necessarily, positioned upstream or 5', of a structural gene region, the expression of which it regulates. Furthermore, the regulatory elements comprising a promoter are usually positioned within 2 kb of the start site of transcription of the gene.

- 10 In the present context, the term "promoter" is also used to describe a synthetic or fusion molecule, or derivative which confers, activates or enhances expression of a nucleic acid molecule in a cell.

Preferred promoters may contain additional copies of one or more specific regulatory 15 elements, to further enhance expression of the sense molecule and/or to alter the spatial expression and/or temporal expression of said sense molecule. For example, regulatory elements which confer copper inducibility may be placed adjacent to a heterologous promoter sequence driving expression of a sense molecule, thereby conferring copper inducibility on the expression of said molecule.

20

Placing a dispersed or foreign nucleic acid molecule under the regulatory control of a promoter sequence means positioning the said molecule such that expression is controlled by the promoter sequence. Promoters are generally positioned 5' (upstream) to the genes that they control. In the construction of heterologous 25 promoter/structural gene combinations it is generally preferred to position the promoter at a distance from the gene transcription start site that is approximately the same as the distance between that promoter and the gene it controls in its natural setting, i.e., the gene from which the promoter is derived. As is known in the art, some variation in this distance can be accommodated without loss of promoter function. Similarly, the 30 preferred positioning of a regulatory sequence element with respect to a heterologous

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gene to be placed under its control is defined by the positioning of the element in its natural setting, i.e., the genes from which it is derived. Again, as is known in the art, some variation in this distance can also occur.

- 5 Examples of promoters suitable for use in the synthetic genes of the present invention include viral, fungal, bacterial, animal and plant derived promoters capable of functioning in plant, animal, insect, fungal, yeast or bacterial cells. The promoter may regulate the expression of the structural gene component constitutively, or differentially with respect to cell, the tissue or organ in which expression occurs or, with respect to
- 10 the developmental stage at which expression occurs, or in response to external stimuli such as physiological stresses, or pathogens, or metal ions, amongst others.

Preferably, the promoter is capable of regulating expression of a nucleic acid molecule in a eukaryotic cell, tissue or organ, at least during the period of time over which the target gene is expressed therein and more preferably also immediately preceding the commencement of detectable expression of the target gene in said cell, tissue or organ.

Accordingly, strong constitutive promoters are particularly preferred for the purposes of the present invention or promoters which may be induced by virus infection or the commencement of target gene expression.

Plant-operable and animal-operable promoters are particularly preferred for use in the synthetic genes of the present invention. Examples of preferred promoters include the bacteriophage T7 promoter, bacteriophage T3 promoter, SP6 promoter, *lac* operator-promoter, *tac* promoter, SV40 late promoter, SV40 early promoter, RSV-LTR promoter, CMV IE promoter, CaMV 35S promoter, SCSV promoter, SCBV promoter and the like.

In consideration of the preferred requirement for high-level expression which coincides with expression of the target gene or precedes expression of the target gene, it is

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highly desirable that the promoter sequence is a constitutive strong promoter such as the CMV-IE promoter or the SV40 early promoter sequence, the SV40 late promoter sequence, the CaMV 35S promoter, or the SCBV promoter, amongst others. Those skilled in the art will readily be aware of additional promoter sequences other than  
5 those specifically described.

In the present context, the terms "in operable connection with" or "operably under the control" or similar shall be taken to indicate that expression of the structural gene region or multiple structural gene region is under the control of the promoter sequence  
10 with which it is spatially connected; in a cell, tissue, organ or whole organism.

In a preferred embodiment of the invention, a structural gene region (i.e. dispersed nucleic acid molecule or foreign nucleic acid molecule) or multiple structural gene region is placed operably in connection with a promoter orientation relative to the  
15 promoter sequence, such that when it is transcribed an mRNA product is synthesized which, if translated, is capable of encoding a polypeptide product of the target gene or a fragment thereof.

However, the present invention is not to be limited to the use of such an arrangement  
20 and the invention clearly extends to the use of synthetic genes and genetic constructs wherein the a structural gene region or multiple structural gene region is placed in the "antisense" orientation relative to the promoter sequence, such that at least a part of the mRNA transcription product thereof is complementary to the mRNA encoded by the target gene or a fragment thereof.

25

Clearly, as the dispersed nucleic acid molecule, foreign nucleic acid molecule or multiple structural gene region comprises tandem direct and/or inverted repeat sequences of the target gene, all combinations of the above-mentioned configurations are encompassed by the invention.

30

In an alternative embodiment of the invention, the structural gene region or multiple structural gene region is operably connected to both a first promoter sequence and a second promoter sequence, wherein said promoters are located at the distal and proximal ends thereof such that at least one unit of said a structural gene region or 5 multiple structural gene region is placed in the "sense" orientation relative to the first promoter sequence and in the "antisense" orientation relative to the second promoter sequence. According to this embodiment, it is also preferred that the first and second promoters be different, to prevent competition there between for cellular transcription factors which bind thereto. The advantage of this arrangement is that the effects of 10 transcription from the first and second promoters in reducing target gene expression in the cell may be compared to determine the optimum orientation for each nucleotide sequence tested.

The synthetic gene preferably contains additional regulatory elements for efficient 15 transcription, for example a transcription termination sequence.

The term "terminator" refers to a DNA sequence at the end of a transcriptional unit which signals termination of transcription. Terminators are 3'-non-translated DNA sequences containing a polyadenylation signal, which facilitates the addition of 20 polyadenylate sequences to the 3'-end of a primary transcript. Terminators active in plant cells are known and described in the literature. They may be isolated from bacteria, fungi, viruses, animals and/or plants or synthesized *de novo*.

As with promoter sequences, the terminator may be any terminator sequence which 25 is operable in the cells, tissues or organs in which it is intended to be used.

Examples of terminators particularly suitable for use in the synthetic genes of the present invention include the SV40 polyadenylation signal, the HSV TK polyadenylation signal, the CYC1 terminator, ADH terminator, SPA terminator, 30 nopaline synthase (NOS) gene terminator of *Agrobacterium tumefaciens*, the

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terminator of the Cauliflower mosaic virus (CaMV) 35S gene, the *zein* gene terminator from *Zea mays*, the Rubisco small subunit gene (SSU) gene terminator sequences, subclover stunt virus (SCSV) gene sequence terminators, any *rho*-independent *E.coli* terminator, or the *lacZ* alpha terminator, amongst others.

5

In a particularly preferred embodiment, the terminator is the SV40 polyadenylation signal or the HSV TK polyadenylation signal which are operable in animal cells, tissues and organs, octopine synthase (OCS) or nopaline synthase (NOS) terminator active in plant cells, tissues or organs, or the *lacZ* alpha terminator which is active in 10 prokaryotic cells.

Those skilled in the art will be aware of additional terminator sequences which may be suitable for use in performing the invention. Such sequences may readily be used without any undue experimentation.

15

Means for introducing (i.e. transfecting or transforming) cells with the synthetic genes described herein or a genetic construct comprising same are well-known to those skilled in the art.

20 In a further alternative embodiment, a genetic construct is used which comprises two or more structural gene regions or multiple structural gene regions wherein each of said structural gene regions is placed operably under the control of its own promoter sequence. As with other embodiments described herein, the orientation of each structural gene region may be varied to maximise its modulatory effect on target gene  
25 expression.

According to this embodiment, the promoters controlling expression of the structural gene unit are preferably different promoter sequences, to reduce competition there between for cellular transcription factors and RNA polymerases. Preferred promoters  
30 are selected from those referred to *supra*.

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Those skilled in the art will know how to modify the arrangement or configuration of the individual structural genes as described *supra* to regulate their expression from separate promoter sequences.

5 The synthetic genes described *supra* are capable of being modified further, for example by the inclusion of marker nucleotide sequences encoding a detectable marker enzyme or a functional analogue or derivative thereof, to facilitate detection of the synthetic gene in a cell, tissue or organ in which it is expressed. According to this embodiment, the marker nucleotide sequences will be present in a translatable format  
10 and expressed, for example as a fusion polypeptide with the translation product(s) of any one or more of the structural genes or alternatively as a non-fusion polypeptide.

Those skilled in the art will be aware of how to produce the synthetic genes described herein and of the requirements for obtaining the expression thereof, when so desired,  
15 in a specific cell or cell-type under the conditions desired. In particular, it will be known to those skilled in the art that the genetic manipulations required to perform the present invention may require the propagation of a genetic construct described herein or a derivative thereof in a prokaryotic cell such as an *E. coli* cell or a plant cell or an animal cell.

20

The synthetic genes of the present invention may be introduced to a suitable cell, tissue or organ without modification as linear DNA in the form of a genetic construct, optionally contained within a suitable carrier, such as a cell, virus particle or liposome, amongst others. To produce a genetic construct, the synthetic gene of the invention  
25 is inserted into a suitable vector or episome molecule, such as a bacteriophage vector, viral vector or a plasmid, cosmid or artificial chromosome vector which is capable of being maintained and/or replicated and/or expressed in the host cell, tissue or organ into which it is subsequently introduced.

30 Accordingly a further aspect of the invention provides a genetic construct which at

least comprises the synthetic gene according to any one or more of the embodiments described herein and one or more origins of replication and/or selectable marker gene sequences.

- 5 Genetic constructs are particularly suitable for the transformation of a eukaryotic cell to introduce novel genetic traits thereto, in addition to the provision of resistance characteristics to viral pathogens. Such additional novel traits may be introduced in a separate genetic construct or, alternatively on the same genetic construct which comprises the synthetic genes described herein. Those skilled in the art will recognise
- 10 the significant advantages, in particular in terms of reduced genetic manipulations and tissue culture requirements and increased cost-effectiveness, of including genetic sequences which encode such additional traits and the synthetic genes described herein in a single genetic construct.
- 15 Usually, an origin of replication or a selectable marker gene suitable for use in bacteria is physically-separated from those genetic sequences contained in the genetic construct which are intended to be expressed or transferred to a eukaryotic cell, or integrated into the genome of a eukaryotic cell.
- 20 In a particularly preferred embodiment, the origin of replication is functional in a bacterial cell and comprises the pUC or the ColE1 origin or alternatively the origin of replication is operable in a eukaryotic cell, tissue and more preferably comprises the 2 micron ( $2\mu\text{m}$ ) origin of replication or the SV40 origin of replication.
- 25 As used herein, the term "selectable marker gene" includes any gene which confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells which are transfected or transformed with a genetic construct of the invention or a derivative thereof.
- 30 Suitable selectable marker genes contemplated herein include the ampicillin-resistance

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gene ( $\text{Amp}^r$ ), tetracycline-resistance gene ( $\text{Tc}^r$ ), bacterial kanamycin-resistance gene ( $\text{Kan}^r$ ), is the zeocin resistance gene (Zeocin is a drug of bleomycin family which is trademark of InVitrogen Corporation), the *AU $\beta$ I-C* gene which confers resistance to the antibiotic aureobasidin A, phosphinothricin-resistance gene, neomycin 5 phosphotransferase gene (*np $\beta$ II*), hygromycin-resistance gene,  $\beta$ -glucuronidase (GUS) gene, chloramphenicol acetyltransferase (CAT) gene, green fluorescent protein-encoding gene or the luciferase gene, amongst others.

Preferably, the selectable marker gene is the *np $\beta$ II* gene or  $\text{Kan}^r$  gene or green 10 fluorescent protein (GFP)-encoding gene.

Those skilled in the art will be aware of other selectable marker genes useful in the performance of the present invention and the subject invention is not limited by the nature of the selectable marker gene.

15 The present invention extends to all genetic constructs essentially as described herein, which include further genetic sequences intended for the maintenance and/or replication of said genetic construct in prokaryotes or eukaryotes and/or the integration of said genetic construct or a part thereof into the genome of a eukaryotic cell or 20 organism.

As with dispersed or foreign nucleic acid molecules, standard methods described 25 *supra* may be used to introduce synthetic genes and genetic constructs into the cell, tissue or organ for the purposes of modulating the expression of the target gene, for example liposome-mediated transfection or transformation, transformation of cells with attenuated virus particles or bacterial cells, cell mating, transformation or transfection procedures known to those skilled in the art or described by Ausubel *et al.* (1992).

Additional means for introducing recombinant DNA into plant tissue or cells include, 30 but are not limited to, transformation using  $\text{CaCl}_2$  and variations thereof, in particular

the method described by Hanahan (1983), direct DNA uptake into protoplasts (Krens *et al.*, 1982; Paszkowski *et al.*, 1984), PEG-mediated uptake to protoplasts (Armstrong *et al.*, 1990) microparticle bombardment, electroporation (Fromm *et al.*, 1985), microinjection of DNA (Crossway *et al.*, 1986), microparticle bombardment of tissue 5 explants or cells (Christou *et al.*, 1988; Sanford, 1988), vacuum-infiltration of tissue with nucleic acid, or in the case of plants, T-DNA-mediated transfer from *Agrobacterium* to the plant tissue as described essentially by An *et al.*(1985), Herrera-Estrella *et al.* (1983a, 1983b, 1985).

- 10 For microparticle bombardment of cells, a microparticle is propelled into a cell to produce a transformed cell. Any suitable ballistic cell transformation methodology and apparatus can be used in performing the present invention. Exemplary apparatus and procedures are disclosed by Stomp *et al.* (U.S. Patent No. 5,122,466) and Sanford and Wolf (U.S. Patent No. 4,945,050). When using ballistic transformation procedures, the 15 genetic construct may incorporate a plasmid capable of replicating in the cell to be transformed.

Examples of microparticles suitable for use in such systems include 1 to 5  $\mu\text{m}$  gold spheres. The DNA construct may be deposited on the microparticle by any suitable 20 technique, such as by precipitation.

In a further embodiment of the present invention, the synthetic genes and genetic constructs described herein are adapted for integration into the genome of a cell in which it is expressed. Those skilled in the art will be aware that, in order to achieve 25 integration of a genetic sequence or genetic construct into the genome of a host cell, certain additional genetic sequences may be required. In the case of plants, left and right border sequences from the T-DNA of the *Agrobacterium tumefaciens* Ti plasmid will generally be required.

- 30 The present invention further extends to an isolated cell, tissue or organ comprising

- 40 -

the synthetic gene described herein or a genetic construct comprising same. The present invention extends further to regenerated tissues, organs and whole organisms derived from said cells, tissues and organs and to propagules and progeny thereof.

5 For example, plants may be regenerated from transformed plant cells or tissues or organs on hormone-containing media and the regenerated plants may take a variety of forms, such as chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., a transformed root stock grafted to an  
10 untransformed scion in citrus species). Transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plants may be selfed to give homozygous second generation (or T2) transformed plants, and the T2 plants further propagated through classical breeding techniques.

15

The present invention is further described with reference to the following non-limiting Examples.

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## EXAMPLE 1

### Genetic constructs comprising BEV polymerase gene sequences linked to the CMV promoter sequence and/or the SV40L promoter sequence

5

#### **1. Commercial Plasmids**

##### **Plasmid pBluescript II (SK+)**

Plasmid pBluescript II (SK+) is commercially available from Stratagene and comprises the LacZ promoter sequence and *lacZ*-alpha transcription terminator, with a multiple 10 cloning site for the insertion of structural gene sequences therein. The plasmid further comprises the ColE1 and f1 origins of replication and ampicillin-resistance gene.

##### **Plasmid pSVL**

Plasmid pSVL is commercially-obtainable from Pharmacia and serves as a source of 15 the SV40 late promoter sequence. The nucleotide sequence of pSVL is also publicly available as GenBank Accession Number U13868.

##### **Plasmid pCR2.1**

Plasmid pCR2.1 is commercially available from Invitrogen and comprises the LacZ 20 promoter sequence and *lacZ*- $\alpha$  transcription terminator, with a cloning site for the insertion of structural gene sequences there between. Plasmid pCR2.1 is designed to clone nucleic acid fragments by virtue of the A-overhang frequently synthesized by Taq polymerase during the polymerase chain reaction. PCR fragments cloned in this fashion are flanked by two EcoRI sites. The plasmid further comprises the ColE1 and 25 f1 origins of replication and kanamycin-resistance and ampicillin-resistance genes.

##### **Plasmid pEGFP-N1 MCS**

Plasmid pEGFP-N1 MCS (Figure 1; Clontech) contains the CMV IE promoter operably connected to an open reading frame encoding a red-shifted variant of wild-type green 30 fluorescent protein (GFP; Prasher *et al.*, 1992; Chalfie *et al.*, 1994; Inouye and Tsui,

1994), which has been optimised for brighter fluorescence. The specific GFP variant encoded by pEGFP-N1 MCS has been disclosed by Cormack *et al.* (1996). Plasmid pEGFP-N1 MCS contains a multiple cloning site comprising *Bgl*II and *Bam*HI sites and many other restriction endonuclease cleavage sites, located between the CMV IE 5 promoter and the GFP open reading frame. Structural genes cloned into the multiple cloning site will be expressed at the transcriptional level if they lack a functional translation start site, however such structural gene sequences will not be expressed at the protein level (i.e. translated). Structural gene sequences inserted into the multiple cloning site which comprise a functional translation start site will be expressed 10 as GFP fusion polypeptides if they are cloned in-frame with the GFP-encoding sequence. The plasmid further comprises an SV40 polyadenylation signal downstream of the GFP open reading frame to direct proper processing of the 3'-end of mRNA transcribed from the CMV-IE promoter sequence. The plasmid further comprises the SV40 origin of replication functional in animal cells; the neomycin-resistance gene 15 comprising SV40 early promoter (SV40 EP in Figure 1) operably connected to the neomycin/kanamycin-resistance gene derived from Tn5 (Kan/neo in Figure 1) and the HSV thymidine kinase polyadenylation signal (HSV TK poly (A) in Figure 1), for selection of transformed cells on kanamycin, neomycin or G418; the pUC19 origin of replication which is functional in bacterial cells (pUC Ori in Figure 1); and the f1 origin 20 of replication for single-stranded DNA production (f1 Ori in Figure 1).

## **2. Expression cassettes**

### **Plasmid pCMV.cass**

Plasmid pCMV.cass (Figure 2) is an expression cassette for driving expression of a 25 structural gene sequence under control of the CMV-IE promoter sequence. Plasmid pCMV.cass was derived from pEGFP-N1 MCS by deletion of the GFP open reading frame as follows: Plasmid pEGFP-N1 MCS was digested with *Pin*AI and *Not* I, blunted-ended using *Pfu*I polymerase and then re-ligated. Structural gene sequences are cloned into pCMV.cass using the multiple cloning site, which is identical to the multiple 30 cloning site of pEGFP-N1 MCS, except it lacks the *Pin*AI site.

**Plasmid pCMV.SV40L.cass**

Plasmid pCMV.SV40L.cass (Figure 3) comprises the synthetic poly A site and the SV40 late promoter sequence from plasmid pCR.SV40L (Figure 4), sub-cloned as a *Sa*/*I* fragment, into the *Sa*/*I* site of plasmid pCMV.cass (Figure 2), such that the CMV-  
5 IE promoter and SV40 late promoter sequences are capable of directing transcription  
in the same direction. Accordingly, the synthetic poly(A) site at the 5' end of the SV40  
promoter sequence is used as a transcription terminator for structural genes expressed  
from the CMV IE promoter in this plasmid, which also provides for the insertion of said  
structural gene via the multiple cloning site present between the SV40 late promoter  
10 and the synthetic poly(A) site (Figure 5). The multiple cloning sites are located behind  
the CMV-IE and SV40 late promoters, including *Bam*H*I* and *Bg**II* sites.

**Plasmid pCMV.SV40LR.cass**

Plasmid pCMV.SV40LR.cass (Figure 4) comprises the SV40 late promoter sequence  
15 derived from plasmid pCR.SV40L, sub-cloned as a *Sa*/*I* fragment into the *Sa*/*I* site of  
the plasmid pCMV.cass (Figure 2), such that the CMV-IE or the SV40 late promoter  
may drive transcription of a structural gene or a multiple structural gene unit, in the  
sense or antisense orientation, as desired. A multiple cloning site is positioned  
between the opposing CMV- IE and SV40 late promoter sequences in this plasmid to  
20 facilitate the introduction of a structural gene sequence. In order for expression of a  
structural gene sequence to occur from this plasmid, it must be introduced with its own  
transcription termination sequence located at the 3' end, because there are no  
transcription termination sequences located between the opposing CMV- IE and SV40  
late promoter sequences in this plasmid. Preferably, the structural gene sequence or  
25 multiple structural gene unit which is to be introduced into pCMV.SV40LR.cass will  
comprise both a 5' and a 3' polyadenylation signal as follows:

- (i) where the structural gene sequence or multiple structural gene unit is  
to be expressed in the sense orientation from the CMV IE promoter sequence  
and/or in the antisense orientation from the SV40 late promoter, the 5'  
30 polyadenylation signal will be in the antisense orientation and the 3'

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polyadenylation signal will be in the sense orientation; and  
(ii) where the structural gene sequence or multiple structural gene unit is to be expressed in the antisense orientation from the CMV IE promoter sequence and/or in the sense orientation from the SV40 late promoter, the 5' 5 polyadenylation signal will be in the sense orientation and the 3' polyadenylation signal will be in the antisense orientation.

Alternatively or in addition, suitably-oriented terminator sequences may be placed at the 5'-end of the CMV and SV40L promoters, as shown in Figure 4.

10

Alternatively, plasmid pCMV.SV40LR.cass is further modified to produce a derivative plasmid which comprises two polyadenylation signals located between the CMV IE and SV40 late promoter sequences, in appropriate orientations to facilitate expression of any structural gene located therebetween in the sense or antisense orientation from either 15 the CMV IE promoter or the SV40 promoter sequence. The present invention clearly encompasses such derivatives.

Alternatively appropriately oriented terminators could be placed upstream of the CMV and SV40L promoters such that transcriptional termination could occur after 20 readthrough of each of the two promoters in the antisense orientation.

### **3. Intermediate Constructs**

#### **Plasmid pCR.Bgl-GFP-Bam**

Plasmid pCR.Bgl-GFP-Bam (Figure 5) comprises an internal region of the GFP open 25 reading frame derived from plasmid pEGFP-N1 MCS (Figure 1) placed operably under the control of the lacZ promoter. To produce this plasmid, a region of the GFP open reading frame was amplified from pEGFP-N1 MCS using the amplification primers Bgl-GFP and GFP-Bam and cloned into plasmid pCR2.1. The internal GFP-encoding region in plasmid pCR.Bgl-GFP-Bam lacks functional translational start and stop 30 codons.

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#### **Plasmid pBSII(SK+).EGFP**

Plasmid pBSII(SK+).EGFP (Figure 6) comprises the EGFP open reading frame derived from plasmid pEGFP-N1 MCS (Figure 1) placed operably under the control of the *lacZ* promoter. To produce this plasmid, the EGFP encoding region of pEGFP-N1 MCS 5 was excised as a *Not*1/*Xho*1 fragment and cloned into the *Not*1/*Xho*1 cloning sites of plasmid pBluescript II (SK+).

#### **Plasmid pCMV.EGFP**

Plasmid pCMV.EGFP (Figure 7) is capable of expressing the EGFP structural gene 10 under the control of the CMV-IE promoter sequence. To produce this plasmid the EGFP sequence from plasmid pBSII(SK+).EGFP was excised as *Bam*H1/*Sac*I fragment and cloned into the *Bg*II/*Sac*I sites of plasmid pCMV.cass (Figure 2).

#### **Plasmid pCR.SV40L**

15 Plasmid pCR.SV40L (Figure 8) comprises the SV40 late promoter derived from plasmid pSVL (GenBank Accession No. U13868; Pharmacia), cloned into pCR2.1 (Stratagene). To produce this plasmid, the SV40 late promoter was amplified using the primers SV40-1 and SV40-2 which comprise *Sa*I cloning sites to facilitate sub-cloning of the amplified DNA fragment into pCMV.cass. The primer also contains a 20 synthetic poly (A) site at the 5' end, such that the amplicification product comprises the synthetic poly(A) site at the 5' end of the SV40 promoter sequence.

#### **Plasmid pCR.BEV.1**

The BEV RNA-dependent RNA polymerase coding region was amplified as a 1,385 25 bp DNA fragment from a full-length cDNA clone encoding same, using primers designated BEV-1 and BEV-2, under standard amplification conditions. The amplified DNA contained a 5'-*Bgl* II restriction enzyme site, derived from the BEV-1 primer sequence and a 3'*Bam*H1 restriction enzyme site, derived from the BEV-2 primer sequence. Additionally, as the BEV-1 primer sequence contains a translation start 30 signal 5'-ATG-3' engineered at positions 15-17, the amplified BEV polymerase

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structural gene comprises the start site in-frame with BEV polymerase-encoding nucleotide sequences. Thus, the amplified BEV polymerase structural gene comprises the ATG start codon immediately upstream (ie. juxtaposed) to the BEV polymerase-encoding sequence. There is no translation stop codon in the amplified DNA. This  
5 plasmid is present as Figure 9.

#### **Plasmid pCR.BEV.2**

The complete BEV polymerase coding region was amplified from a full-length cDNA clone encoding same, using primers BEV-1 and BEV-3. Primer BEV-3 comprises a  
10 *Bam*HI restriction enzyme site at positions 5 to 10 inclusive and the complement of a translation stop signal at positions 11 to 13. As a consequence, an open reading frame comprising a translation start signal and translation stop signal, contained between the *Bg*/II and *Bam*HI restriction sites. The amplified fragment was cloned into pCR2.1 (Stratagene) to produce plasmid pCR2.BEV.2 (Figure 10).

15

#### **Plasmid pCR.BEV.3**

A non-translatable BEV polymerase structural gene was amplified from a full-length BEV polymerase cDNA clone using the amplification primers BEV-3 and BEV-4. Primer BEV-4 comprises a *Bg*/II cloning site at positions 5-10 and sequences  
20 downstream of this *Bg*/II site are homologous to nucleotide sequences of the BEV polymerase gene. There is no functional ATG start codon in the amplified DNA product of primers BEV-3 and BEV-4. The BEV polymerase is expressed as part of a polyprotein and, as a consequence, there is no ATG translation start site in this gene. The amplified DNA was cloned into plasmid pCR2.1 (Stratagene) to yield  
25 plasmid pCR.BEV.3 (Figure 11).

#### **Plasmid pCMV.EGFP.BEV2**

Plasmid pCMV.EGFP.BEV2 (Figure 12) was produced by cloning the BEV polymerase sequence from pCR.BEV.2 as a *Bg*III/*Bam*HI fragment into the *Bam*HI site of  
30 pCMV.EGFP.

#### **4. Control Plasmids**

##### **Plasmid pCMV.BEV.2**

Plasmid pCMV.BEV.2 (Figure 13) is capable of expressing the entire BEV polymerase open reading frame under the control of CMV-IE promoter sequence. To produce pCMV.BEV.2, the BEV polymerase sequence from pCR.BEV.2 was sub-cloned in the sense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bgl*II/*Bam*HI-digested pCMV.cass (Figure 2).

##### **Plasmid pCMV.BEV.3**

10 Plasmid pCMV.BEV.3 (Figure 14) expresses a non-translatable BEV polymerase structural gene in the sense orientation under the control of the CMV-IE promoter sequence. To produce pCMV.BEVnt, the BEV polymerase sequence from pCR.BEV.3 was sub-cloned in the sense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bgl*II/*Bam*HI-digested pCMV.cass (Figure 2).

15

##### **Plasmid pCMV.VEB**

Plasmid pCMV.VEB (Figure 15) expresses an antisense BEV polymerase mRNA under the control of the CMV-IE promoter sequence. To produce plasmid pCMV.VEB, the BEV polymerase sequence from pCR.BEV.2 was sub-cloned in the antisense 20 orientation as a *Bgl*II-to-*Bam*HI fragment into *Bgl*II/*Bam*HI-digested pCMV.cass (Figure 2).

##### **Plasmid pCMV.BEV.GFP**

Plasmid pCMV.BEV.GFP (Figure 16) was constructed by cloning the GFP fragment 25 from pCR.Bgl-GFP-Bam as a *Bgl*II/*Bam*HI fragment into *Bam*HI-digested pCMV.BEV.2. This plasmid serves as a control in some experiments and also as an intermediate construct.

##### **Plasmid pCMV.BEV.SV40-L**

30 Plasmid pCMV.BEV.SV40-L (Figure 17) comprises a translatable BEV polymerase

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structural gene derived from plasmid pCR.BEV.2 inserted in the sense orientation between the CMV-IE promoter and the SV40 late promoter sequences of plasmid pCMV.SV40L.cass. To produce plasmid pCMV.BEV.SV40L-O, the BEV polymerase structural gene was sub-cloned as a *Bg*/II-to-*Bam*HI fragment into *Bg*/II-digested 5 pCMV.SV40L.cass DNA.

#### **Plasmid pCMV.O.SV40L.BEV**

Plasmid pCMV.O.SV40L.BEV (Figure 18) comprises a translatable BEV polymerase structural gene derived from plasmid pCR.BEV.2 cloned downstream of tandem CMV-10 IE promoter and SV40 late promoter sequences present in plasmid pCMV.SV40L.cass. To produce plasmid pCMV.O.SV40L.BEV, the BEV polymerase structural gene was sub-cloned in the sense orientation as a *Bg*/II-to-*Bam*HI fragment into *Bam*HI-digested pCMV.SV40L.cass DNA.

#### **15 Plasmid pCMV.O.SV40L.VEB**

Plasmid pCMV.O.SV40L.VEB (Figure 19) comprises an antisense BEV polymerase structural gene derived from plasmid pCR.BEV.2 cloned downstream of tandem CMV-IE promoter and SV40 late promoter sequences present in plasmid pCMV.SV40L.cass. To produce plasmid pCMV.O.SV40L.VEB, the BEV polymerase 20 structural gene was sub-cloned in the antisense orientation as a *Bg*/II-to-*Bam*HI fragment into *Bam*HI-digested pCMV.SV40L.cass DNA.

#### **5. Test Plasmids**

##### **Plasmid pCMV.BEVx2**

25 Plasmid pCMV.BEVx2 (Figure 20) comprises a direct repeat of a complete BEV polymerase open reading frame under the control of the CMV-IE promoter sequence. In eukaryotic cells at least, the open reading frame located nearer the CMV-IE promoter is translatable. To produce pCMV.BEVx2, the BEV polymerase structural gene from plasmid pCR.BEV.2 was sub-cloned in the sense orientation as a *Bg*/II-to-30 *Bam*HI fragment into *Bam*HI-digested pCMV.BEV.2, immediately downstream of the

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BEV polymerase structural gene already present therein.

**Plasmid pCMV.BEVx3**

Plasmid pCMV.BEVx3 (Figure 21) comprises a direct repeat of three complete BEV 5 polymerase open reading frames under the control of the CMV-1E promoter. To produce pCMV.BEVx3, the BEV polymerase fragment from pCR.BEV.2 was cloned in the sense orientation as a BgIII/BamHI fragment into the BamHI site of pCMV.BEVx2, immediately downstream of the BEV polymerase sequences already present therein.

10

**Plasmid pCMV.BEVx4**

Plasmid pCMV.BEVx4 (Figure 22) comprises a direct repeat of four complete BEV 15 polymerase open reading frames under the control of the CMV-1E promoter. To produce pCMV.BEVx4, the BEV polymerase fragment from pCR.BEV.2 was cloned in the sense orientation as a BgIII/BamHI fragment into the BamHI site of pCMV.BEVx3, immediately downstream of the BEV polymerase sequences already present therein.

**Plasmid pCMV.BEV.SV40L.BEV**

20 Plasmid pCMV.BEV.SV40L.BEV (Figure 23) comprises a multiple structural gene unit comprising two BEV polymerase structural genes placed operably and separately under control of the CMV-IE promoter and SV40 late promoter sequences. To produce plasmid pCMV.BEV.SV40L.BEV, the translatable BEV polymerase structural gene present in pCR.BEV.2 was sub-cloned in the sense orientation as a BgII-to- 25 BamHI fragment behind the SV40 late promoter sequence present in BamHI-digested pCMV.BEV.SV40L-O.

**Plasmid pCMV.BEV.SV40L.VEB**

Plasmid pCMV.BEV.SV40L.VEB (Figure 24) comprises a multiple structural gene unit 30 comprising two BEV polymerase structural genes placed operably and separately

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under control of the CMV-IE promoter and SV40 late promoter sequences. To produce plasmid pCMV.BEV.SV40L.VEB, the translatable BEV polymerase structural gene present in pCR.BEV.2 was sub-cloned in the antisense orientation as a *Bg*II-to-*Bam*HI fragment behind the SV40 late promoter sequence present in *Bam*HI-digested 5 pCMV.BEV.SV40L-O. In this plasmid, the BEV polymerase structural gene is expressed in the sense orientation under control of the CMV-IE promoter to produce a translatable mRNA, whilst the BEV polymerase structural gene is also expressed under control of the SV40 promoter to produce an antisense mRNA species.

#### 10 Plasmid pCMV.BEV.GFP.VEB

Plasmid pCMV.BEV.GFP.VEB (Figure 25) comprises a BEV structural gene inverted repeat or palindrome, interrupted by the insertion of a GFP open reading frame (stuffer fragment) between each BEV structural gene sequence in the inverted repeat. To produce plasmid pCMV.BEV.GFP.VEB, the GFP stuffer fragment from pCR.Bgl-GFP-15 *Bam* was first sub-cloned in the sense orientation as a *Bg*II-to-*Bam*HI fragment into *Bam*HI-digested pCMV.BEV.2 to produce an intermediate plasmid pCMV.BEV.GFP wherein the BEV polymerase-encoding and GFP-encoding sequences are contained within the same 5'-*Bg*II-to-*Bam*HI-3' fragment. The BEV polymerase structural gene from pCMV.BEV.2 was then cloned in the antisense orientation as a *Bg*II-to-*Bam*HI 20 fragment into *Bam*HI-digested pCMV.BEV.GFP. The BEV polymerase structural gene nearer the CMV-IE promoter sequence in plasmid pCMV.BEV.GFP.VEB is capable of being translated, at least in eukaryotic cells.

#### Plasmid pCMV.EGFP.BEV2.PFG

25 Plasmid pCMV.EGFP.BEV2.PFG (Figure 26) comprise a GFP palindrome, interrupted by the insertion of a BEV polymerase sequence between each GFP structural gene in the inverted repeat. To produce this plasmid the GFP fragment from pCR.Bgl-GFP-*Bam* was cloned as a *Bg*III/*Bam*HI fragment into the *Bam*HI site of pCMV.EGFP.BEV2 in the antisense orientation relative to the CMV promoter.

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### **Plasmid pCMV.BEV.SV40LR**

Plasmid pCMV.BEV.SV40LR (Figure 27) comprises a structural gene comprising the entire BEV polymerase open reading frame placed operably and separately under control of opposing CMV-IE promoter and SV40 late promoter sequences, thereby 5 potentially producing BEV polymerase transcripts at least from both strands of the full-length BEV polymerase structural gene. To produce plasmid pCMV.BEV.SV40LR, the translatable BEV polymerase structural gene present in pCR.BEV.2 was sub-cloned, as a *Bg*II-to-*Bam*H<sub>I</sub> fragment, into the unique *Bg*II site of plasmid pCMV.SV40LR.cass, such that the BEV open reading frame is present in the sense 10 orientation relative to the CMV-IE promoter sequence.

Those skilled in the art will recognise that it is possible to generate a plasmid wherein the BEV polymerase fragment from pCR.BEV.2 is inserted in the antisense orientation, relative to the CMV IE promoter sequence, using this cloning strategy. The present 15 invention further encompasses such a genetic construct.

## **EXAMPLE 2**

**Genetic constructs comprising the porcine  $\alpha$ -1,3-galactosyltransferase  
(Galt) structural gene sequence or sequences operably connected  
20 to the CMV promoter sequence and/or the SV40L promoter sequence**

### **1. Commercial Plasmids**

#### **Plasmid pcDNA3**

Plasmid pcDNA3 is commercially available from Invitrogen and comprises the CMV-IE 25 promoter and BGHpA transcription terminator, with multiple cloning sites for the insertion of structural gene sequences there between. The plasmid further comprises the ColE1 and fI origins of replication and neomycin-resistance and ampicillin-resistance genes.

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## **2. Intermediate plasmids**

### **Plasmid pcDNA3.Galt**

Plasmid pcDNA3.Galt (BresaGen Limited, South Australia, Australia; Figure 28) is plasmid pcDNA3 (Invitrogen) and comprises the cDNA sequence encoding porcine 5 gene alpha-1,3-galactosyltransferase (Galt) operably under the control of the CMV-IE promoter sequence such that it is capable of being expressed therefrom. To produce plasmid pcDNA3.Galt, the porcine gene alpha-1,3-galactosyltransferase cDNA was cloned as an *Eco*RI fragment into the *Eco*RI cloning site of pcDNA3. The plasmid further comprises the *ColE1* and *f1* origins of replication and the neomycin and 10 ampicillin-resistance genes.

## **3. Control Plasmids**

### **Plasmid pCMV.Galt**

Plasmid pCMV.Galt (Figure 29) is capable of expressing the Galt structural gene under 15 the control of the CMV-IE promoter sequence. To produce plasmid pCMV.Galt, the Galt sequence from plasmid pcDNA3.Galt was excised as an *Eco*RI fragment and cloned in the sense orientation into the *Eco*RI site of plasmid pCMV.cass (Figure 2).

### **Plasmid pCMV.EGFP.Galt**

20 Plasmid pCMV.EGFP.Galt (Figure 30) is capable of expressing the Galt structural gene as a Galt fusion polypeptide under the control of the CMV-IE promoter sequence. To produce plasmid pCMV.EGFP.Galt, the Galt sequence from pCMV.Galt (Figure 29) was excised as a *Bgl*II/*Bam*HI fragment and cloned into the *Bam*HI site of pCMV.EGFP.

25

### **Plasmid pCMV.Galt.GFP**

Plasmid pCMV.Galt.GFP (Figure 31) was produced by cloning the Galt cDNA as an *Eco*RI fragment from pcDNA3 into *Eco*RI-digested pCMV.EGFP in the sense orientation. This plasmid serves as both a control and construct intermediate.

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#### **Plasmid pCMV.Galt.SV40L.0**

The plasmid pCMV.Galt.SV40L.0 (Figure 32) comprises a Galt structural gene cloned downstream of the CMV promoter present in pCMV.SV40L.cass. To produce the plasmid the Galt cDNA fragment from pCMV.Galt was cloned as a BgIII/BamHI into 5 BgIII-digested pCMV.SV40L.cass in the sense orientation.

#### **Plasmid pCMV.O.SV40L.tlaG**

The plasmid pCMV.O.SV40L.tlaG (Figure 33) comprises a Galt structural gene clones in an antisense orientation downstream of the SV40L promoter present in 10 pCMV.SV40L.cass. To produce this plasmid the Galt cDNA fragment from pCMV.Galt was cloned as a BgIII/BamHI into BamHI-digested pCMV.SV40L.cass in the antisense orientation.

#### **Plasmid pCMV.O.SV40L.Galt**

15 The plasmid pCMV.O.SV40L.Galt (Figure 34) comprises a Galt structural gene cloned downstream of the SV40L promoter present in pCMV.SV40L.cass. To produce the plasmid the Galt cDNA fragment from pCMV.Galt was cloned as a BgIII/BamHI into BamHI-digested pCMV.SV40L.cass in the sense orientation.

### **20 4. Test Plasmids**

#### **Plasmid pCMV.Galtx2**

Plasmid pCMV.Galtx2 (Figure 35) comprises a direct repeat of a Galt open reading frame under the control of the CMV-IE promoter sequence. In eukaryotes cells at least, the open reading frame located nearer the CMV-IE promoter is translatable. To 25 produce pCMV.Galtx2, the Galt structural gene from pCMV.Galt was excised as a BgIII/BamHI fragment and cloned in the sense orientation into the BamHI cloning site of pCMV.Galt.

#### **Plasmid pCMV.Galtx4**

30 Plasmid pCMV.Galtx4 (Figure 36) comprises a quadruple direct repeat of a Galt open

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reading frame under the control of the CMV-IE promoter sequence. In eukaryotes cells at least, the open reading frame located nearer the CMV-IE promoter is translatable. To produce pCMV.Galtx4, the Galtx2 sequence from pCMV.Galtx2 was excised as a *Bgl*II/*Bam*HI fragment and cloned in the sense orientation into the *Bam*HI cloning site 5 of pCMV.Galtx2.

#### **Plasmid pCMV.Galt.SV40L.Galt**

The plasmid pCMV.Galt.SV40L.Galt (Figure 37) is designed to express two sense transcripts of Galt, one driven by the CMV promoter, the other by the SV40L promoter.

10 To produce the plasmid a Galt cDNA fragment from pCMV.Galt was cloned as a *Bgl*III/*Bam*HI fragment into *Bgl*III-digested pCMV.O.SV40.Galt in the sense orientation.

#### **Plasmid pCMV.Galt.SV40L.tlaG**

The plasmid pCMV.Galt.SV40.tlaG (Figure 38) is designed to express a sense transcript of Galt driven by the CMV promoter and an antisense transcript driven by the SV40L promoter. To produce the plasmid a Galt cDNA fragment from pCMV.Galt was cloned as a *Bgl*III/*Bam*HI fragment into *Bgl*III-digested pCMV.O.SV40.talG in the sense orientation.

20 **Plasmid pCMV.Galt.GFP.tlaG**

Plasmid pCMV.Galt.GFP.tlaG (Figure 39) comprise a Galt palindrome, interrupted by the insertion of a GFP sequence between each Galt structural gene in the inverted repeat. To produce this plasmid the *Bgl*III/*Bam*HI Galt cDNA fragment from pCMV.Galt was cloned into the *Bam*HI site of pCMV.Galt.GFP in the antisense relative to the CMV 25 promoter.

#### **Plasmid pCMV.EGFP.Galt.PFG**

The plasmid pCMV.EGFP.Galt.PFG (Figure 40) comprises a GFP palindrome, interrupted by the insertion of a Galt sequence between each GFP structural gene of 30 the inverted repeat, expression of which is driven by the CMV promoter. To produce

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this plasmid the Galt sequences from pCMV.Galt were cloned as a BgIII/BamHI fragment into BamHI-digested pCMV.EGFP in the sense orientation to produce the intermediate pCMV.EGFP.Galt (not shown); following this further GFP sequences from pCR.Bgl-pCMV.EGFP.Galt in the antisense orientation.

5

#### **Plasmid pCMV.Galt.SV40LR**

The plasmid pCMV.Galt.SV40LR (Figure 41) is designed to express Galt cDNA sequences cloned between the opposing CMV and SV40L promoters in the expression cassette pCMV.SV40LR.cass. To produce this plasmid Galt sequences from 10 pCMV.Galt were cloned as a BgIII/BamHI fragment in BgIII-digested pCMV.SV40LR.cass in the sense orientation relative to the 35S promoter.

### **EXAMPLE 3**

**Genetic constructs comprising PVY Nia sequences operably linked to the 35S promoter sequence and/or the SCBV promoter sequence**

**1: Binary vector**

**Plasmid pART27**

Plasmid pART27 is a binary vector, specifically designed to be compatible with the 20 pART7 expression cassette. It contains bacterial origins of replication for both *E. coli* and *Agrobacterium tumefaciens*, a spectinomycin resistance gene for bacterial selection, left and right T-DNA borders for transfer of DNA from *Agrobacterium* to plant cells and a kanamycin resistance cassette to permit selection of transformed plant cells. The kanamycin resistance cassette is located between the T-DNA borders, 25 pART27 also contains a unique NotI restriction site which permits cloning of constructs prepared in vectors such as pART7 to be cloned between the T-DNA borders. Construction of pART27 is described in Gleave, AP (1992).

When cloning NotI inserts into this vector, two insert orientations can be obtained. In 30 all the following examples the same insert orientation, relative to the direction of the

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35S promoter in the described pART7 constructs was chosen; this was done to minimise any experimental artefacts that may arise from comparing different constructs with different insert orientations.

### 5 2. Commercial plasmids

#### **Plasmid pBC (KS-)**

Plasmid pBC (KS-) is commercially available from Stratagene and comprises the LacZ promoter sequence and lacZ-alpha transcription terminator, with a multiple cloning site for the insertion of structural gene sequences therein. The plasmid further comprises  
10 the ColE1 and fl origins of replication and a chloramphenicol-resistance gene.

#### **Plasmid pSP72**

Plasmid pSP72 is commercially available from Promega and contains a multiple cloning site for the insertion of structural gene sequences therein. The plasmid further  
15 comprises the ColE1 origin of replication and an ampicillin-resistance gene.

### 3. Expression cassettes

#### **Plasmid pART7**

Plasmid pART7 is an expression cassette designed to drive expression of sequences  
20 cloned behind the 35S promoter. It contains a polylinker to assist cloning and a region of the octopine synthase terminator. The 35S expression cassette is flanked by two Not I restriction sites which permits cloning into binary expression vectors, such as pART27 which contains a unique NotI site. Its construction as described in Gleave, AP (1992), a map is shown in Figure 43.

25

#### **Plasmid pART7.35S.SCBV.cass**

Plasmid p35S.CMV.cass was designed to express two separate gene sequences cloned into a single plasmid. To create this plasmid, sequences corresponding to the nos terminator and the SCBV promoter were amplified by PCR then cloned in the  
30 polylinker of pART7 between the 35S promoter and OCS.

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The resulting plasmid has the following arrangement of elements:

35S promoter - polylinker 1 - NOS terminator - SCBV promoter - polylinker 2 - OCS terminator.

5

Expression of sequences cloned into polylinker 1 is controlled by the 35S promoter, expression of sequences cloned into polylinker 2 is controlled by the SCBV promoter.

The NOS terminator sequences were amplified from the plasmid pAHC27 (Christensen  
10 and Quail, 1996) using the two oligonucleotides;

NOS 5' (forward primer; SEQ ID ??)

5'-GGATTCCCGGGACGTCGCGAATTCCCCGATCGTTC-3'; and

15 NOS 3' (reverse primer; SEQ ID ??)

5'-CCATGGCCATATAGGCCCGATCTAGAACATAG-3'

Nucleotide residues 1 to 17 for NOS 5' and 1 to 15 for NOS 3' represent additional nucleotides designed to assist in construct preparation by adding additional restriction  
20 sites. For NOS 5' these are BamHI, SmaI, AatII and the first 4 bases of an NruI site,  
for NOS 3' these are NcoI and SfiI sites. The remaining sequences for each oligonucleotide are homologous to the 5' and 3' ends respectively of NOS sequences in pAHC 27.

25 The SCBV promoter sequences were amplified from the plasmid pScBV-20 (Tzafir et al, 1998) using the two oligonucleotides:

SCBV 5': 5'-CCATGGCCTATATGCCATTCCCCACATTCAAG-3'; and

30 SCBV 3': 5'-AACGTTAACTTCTACCCAGTTCCAGAG-3'

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Nucleotide residues 1 to 17 of SCBV 5' encode NcoI and SfiI restriction sites designed to assist in construct preparation, the remaining sequences are homologous to upstream sequences of the SCMV promoter region. Nucleotide residues 1 to 9 of SCBV 3' encode Psp10461 and HpaI restriction sites designed to assist in construct 5 preparation, the remaining sequences are homologous to the reverse and complement of sequences near the transcription initiation site of SCBV.

Sequences amplified from pScBV-20 using PCR and cloned into pCR2.1 (Invitrogen) to produce pCR.NOS and pCR.SCBV respectively. SmaI/SfiI cut pCR.NOS and 10 SfiI/HpaI cut pCR.SCBV were ligated into Sma I cut pART7 and a plasmid with a suitable orientation was chosen and designated pART7.35S.SCBV.cass, a map of this construct is shown in Figure 43.

#### ***4. Intermediate constructs***

##### **15 Plasmid pBC.PVY**

A region of the PVY genome was amplified by PCR using reverse-transcribed RNA isolated from PVY-infected tobacco as a template using standard protocols and cloned into a plasmid pGEM 3 (Stratagene), to create pGEM.PVY. A SalI/HindIII fragment from pGEM.PVY, corresponding to a SalI/HindIII fragment positions 1536-2270 of the 20 PVY strain O sequence (Acc. No D12539, Genbank), was then subcloned into the plasmid pBC (Stratagene Inc.) to create pBC.PVY (Figure 44).

##### **Plasmid pSP72.PVY**

Plasmid pSP72.PVY was prepared by inserting an EcoRI/SalI fragment from pBC.PVY 25 into EcoRI/SalI cut pSP72 (Promega). This construct contains additional restriction sites flanking the PVY insert which were used to assist subsequent manipulations. A map of this construct is shown in Figure 45.

##### **Plasmid ClapBC.PVY**

30 Plasmid ClaI pBC.PVY was prepared by inserting a ClaI/SalI fragment from pSP72.PVY

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into Clal/Sal I cutpBC (Stratagene). This construct contains additional restriction sites flanking the PVY insert which were used to assist subsequent manipulations. A map of this construct is shown in Figure 46.

##### **5 Plasmid pBC.PVYx2**

Plasmid pBC.PVYx2 contains two direct head-to-tail repeats of the PVY sequences derived from pBC.PVY. The plasmid was generated by cloning an Accl/Clal PVY fragment from pSP72.PVY into Accl cut pBC.PVY and is shown in Figure 47.

##### **10 Plasmid pSP72.PVYx2**

Plasmid pSP72.PVYx2 contains two direct head-to-tail repeats of the PVY sequences derived from pBC.PVY. The plasmid was generated by cloning an Accl/Clal PVY fragment from pBc.PVY into Accl cut pSP72.PVY and is shown in Figure 48.

##### **15 Plasmid pBC.PVYx3**

Plasmid pBC.PVYx3 contains three direct head-to-tail repeats of the PVY sequences derived from pBC.PVY. The plasmid was prepared by cloning an Accl/Clal PVY fragment from pSP72.PVY into Accl cut pBC.PVYx2 and is shown in Figure 49.

##### **20 Plasmid pBC.PVYx4**

Plasmid pBC.PVYx4 contains four direct head-to-tail repeats of the PVY sequences derived from pBC.PVY. The plasmid was prepared by cloning the direct repeat of PVY sequences from pSP72.PVYx2 as an Accl/Clal fragment into Accl cut pBC.PVYx2 and is shown in Figure 50.

25

##### **Plasmid pBC.PVY.LNYV**

All attempts to create direct palindromes of PVY sequences failed, presumably such sequence arrangements are unstable in commonly used *E. coli* cloning hosts. Interrupted palindromes however proved stable.

30

- 60 -

To create interrupted palindromes of PVY sequences a "stuffer" fragment of approximately 360 bp was inserted into Cla pBV.PVY downstream of the PVY sequences. The stuffer fragment was made as follows:

- 5 A clone obtained initially from a cDNA library prepared from lettuce necrotic yellows virus (LNYV) genomic RNA (Deitzgen et al, 1989), known to contain the 4b gene of the virus, was amplified by PCR using the primers:

LNYV 1:5'-ATGGGATCCGTTATGCCAAGAAGAAGGA-3'; and

10

LNYV 2:5'-TGTGGATCCCTAACGGACCCGATG-3'

The first 9 nucleotide of these primers encode a BamHI site, the remaining nucleotides are homologous to sequences of the LNYV 4b gene.

15

Following amplification, the fragment was cloned into the EcoRI site of pCR2.1 (Stratagene). This EcoRI fragment was cloned into the EcoRI site of Cla pBC.PVY to create the intermediate plasmid pBC.PVY.LNYV which is shown in Figure 51.

#### 20 Plasmid pBC.PVY.LNYV.PVY

The plasmid pBC.PVY.LNYV.YVP contains an interrupted direct repeat of PVY sequences. To create this plasmid a HpaI/HincII fragment from pSP72 was cloned into SmaI-digested pBC.PVY.LNYV and a plasmid containing the sense orientation isolated, a map of this construct is shown in Figure 52.

25

#### Plasmid pBC.PVY.LNYV.YVP<sub>Δ</sub>

The plasmid pBV.PVY.LNYV.YVP<sub>Δ</sub> contains a partial interrupted palindrome of PVY sequences. One arm of the palindrome contains all the PVY sequences from pBC.PVY, the other arm contains part of the sequences from PVY, corresponding to

30 sequences between the EcoRV and Hincll sites of pSP72.PVY. To create this plasmid

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an EcoRV/HincII fragment from pSP72.PVY was cloned into SmaI-digested pBC.PVY.LNYV and a plasmid containing the desired orientation isolated, a map of this construct is shown in Figure 53.

### 5 Plasmid pBC.PVY.LNYV.YVP

The plasmid pBC.PVY.LNYV.YVP contains an interrupted palindrome of PVY sequences. To create this plasmid a HpaI/HincII fragment from pSP72. was cloned into SmaI-digested pBC.PVY.LNYV and a plasmid containing the antisense orientation isolated, a map of this construct is shown in Figure 54.

10

### 5. *Control plasmids*

#### Plasmids pART7.PVY & pART7.PVY

Plasmid pART7.PVY (Figure 55) was designed to express PVY sequences driven by the 35S promoter. This plasmid serves as a control construct in these experiments, 15 against which all other constructs was compared. To generate this plasmid a C<sub>la</sub>I/A<sub>ccl</sub>I fragment from ClapBC.PVY was cloned into C<sub>la</sub>I-digested pART7 and a plasmid with expected to express a sense PVY sequence with respect to the PVY genome, was selected. Sequences consisting of the 35S promoter, PVY sequences and the OCS 20 terminator were excised as a N<sub>ot</sub>I fragment and cloned into N<sub>ot</sub>I-digested pART27, a plasmid with the desired insert orientation was selected and designated pART27.

#### Plasmids pART7.35S.PVY.SCBV.O & pART27.35S.PVY.SCBV.O

Plasmid pART7.35S.PVY.SCBV.O (Figure 56) was designed to act as a control for co-expression of multiple constructs from a single plasmid in transgenic plants. The 35S 25 promoter was designed to express PVY sense sequences, whilst the SCBV promoter was empty. To generate this plasmid, the PVY fragment from C<sub>la</sub> pBC.PVY was cloned as a X<sub>ba</sub>I/EcoRI fragment into X<sub>ba</sub>I/EcoRI-digested pART7.35S.SCBV.cass to create p35S.PVY.SCBV>O. Sequences consisting of the 35S promoter driving 30 sense PVY sequences and the NOS terminator and the SCBV promoter and OCS terminator were excised as a N<sub>ot</sub>I fragment and cloned into pART27, a plasmid with

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the desired insert orientation was isolated and designated pART27.35S.PVY.SCBV.O.

**Plasmids pART7.35S.O.SCBV.PVY & pART27.35S.O.SCBV.PVY**

Plasmid pART27.35S.O.SCBV.PVY (Figure 57) was designed to act as an additional  
5 control for co-expression of multiple constructs from a single plasmid in transgenic  
plants. No expressible sequences were cloned behind the 35S promoter, whilst the  
SCBV promoter drove expression of a PVY sense fragment. To generate this plasmid,  
the PVY fragment from Cla pBC.PVY was cloned as a Clal fragment into Clal-digested  
pART7.35S.SCBV.cass, a plasmid containing PVY sequences in a sense orientation  
10 was isolated and designated p35S.O.SCBV.PVY. Sequences, consisting of the 35S  
promoter and NOS terminator, the SCBV promoter driving sense PVY sequences and  
the OCS terminator were excised as a NotI fragment and cloned into pART27, a  
plasmid with the desired insert orientation was isolated and designated  
pART27.35S.O.SCBV.PVY.

15

**Plasmids pART7.35S.O.SCBV.YVP & pART7.35S.O.SCBV.YVP**

Plasmid pART7.35S.O.SCBV.YVP (Figure 58) was designed to act as an additional  
control for co-expression of multiple constructs from a single plasmid in transgenic  
plants. No expressible sequences were cloned behind the 35S promoter, whilst the  
20 SCBV promoter drove expression of a PVY antisense fragment. To generate this  
plasmid, the PVY fragment from Cla pBC.PVY was cloned as a Clal fragment into Clal-  
digested p35S.SCBV.cass, a plasmid containing PCY sequences in an antisense  
orientation was isolated and designated p35S.O.SCBV.YVP. Sequences, consisting  
of the 35S promoter and NOS terminator, the SCBV promoter driving sense PVY  
25 sequences and the OCS terminator were excised as a NotI fragment and cloned into  
pART27, a plasmid with the desired insert orientation was isolated and designated  
pART27.35S.O.SCBV.YVP.

**6. Test plasmids**

30 Plasmids pART7.PVYx2 & pART27.PVYx2

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Plasmid pART7.PVYx2 (Figure 59) was designed to express a direct repeat of PVY sequences driven by the 35S promoter in transgenic plants. To generate this plasmid, direct repeats from pBC.PVYx2 were cloned as a Xhol/BamHI fragment into Xhol/BamHI cut pART7. Sequences consisting of the 35 S promoter, direct repeats 5 of PVY and the OCS terminator were excised as a NotI fragment from pART7.PVYx2 and cloned into NotI-digested pART27, a plasmid with the desired insert orientation was selected and designated pART27.PVYx2.

#### **Plasmids pART7.PVYx3 & pART27.PVYx3**

10 Plasmid pART7.PVYx3 (Figure 60) was designed to express a direct repeat of three PVY sequences driven by the 35S promoter in transgenic plants. To generate this plasmid, direct repeats from pBC.PVYx3 were cloned as a Xhol/BamHI fragment into Xhol/BamHI cut pART7. Sequences consisting of the 35S promoter, direct repeats of PVY and OCS terminator were excised as a NotI fragment from pART.PVYx3 and 15 cloned into NotI-digested pART27, a plasmid with the desired insert orientation was selected and designated pART27.PVYx3.

#### **Plasmids pART7.PVYx4 & pART27.PVYx4**

Plasmid pART7.PVYx4 (Figure 61) was designed to express a direct repeat of four 20 PVY sequences driven by the 35S promoter in transgenic plants. To generate this plasmid, direct repeats from pBC.PVYx4 were cloned as a Xhol/BamHI fragment into xhol/BamHI cut pART7. Sequences consisting of the 35S promoter, direct repeats of PVY and the OCS terminator were excised as a NotI fragment from pART7.PVYx3 and cloned into NotI-digested pART27, a plasmid with the desired insert orientation was 25 selected and designated pART27.PVYx3.

#### **Plasmids pART7.PVY.LNYV.PVY & pART27.PVY.LNYV.PVY**

Plasmid pART7.PVY.LNYV.PVY (Figure 62) was designed to express the interrupted direct repeat of PVY sequences driven by the 35S promoter in transgenic plants. This 30 construct was prepared by cloning the interrupted direct repeat of PVY from

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pBC.PVY.LNYV.PVY as a Xhol/XbaI fragment into pART7 digested with Xhol/XbaI. Sequences consisting of the 35S promoter, the interrupted direct repeat of PVY sequences and the OCS terminator were excised from pART7.PVY.LNYV.PVY as a NotI fragment and cloned into NotI-digested pART27, a plasmid with the desired insert 5 orientation was selected and designated pART27.PVY.LNYV.PVY.

**Plasmids pART7.PVY.LNYV.YVP<sub>Δ</sub> & pART27.PVY.LNYV.YVP<sub>Δ</sub>**

Plasmid pART7.PVY.LNYV.YVP<sub>Δ</sub> (Figure 63) was designed to express the partial interrupted palindrome of PVY sequences driven by the 35S promoter in transgenic 10 plants. This construct was prepared by cloning the partial interrupted palindrome of PVY sequences from pBC.PVY.LNYV.YVP<sub>Δ</sub> as a Xhol/XbaI fragment into pART7 digested with Xhol/XbaI. Sequences consisting of the 35S promoter, the partial interrupted palindrome of PVY sequences and the OCS terminator were excised from pART7.PVY.LNYV.YVP<sub>Δ</sub> as a NotI fragment and cloned into NotI-digested pART27, 15 a plasmid with the desired insert orientation was selected and designated pART27.PVY.LNYV.YVP.

**Plasmids pART7.PVY.LNYV.YVP & pART27.PVY.LNYV.YVP**

Plasmid pART7.PVY.LNYV.YVP (Figure 64) was designed to express the interrupted 20 palindrome of PVY sequences driven by the 35S promoter in transgenic plants. This construct was prepared by cloning the interrupted palindrome of PVY sequences from pBC.PVY.LNYV.YVP<sub>Δ</sub> as a Xhol/XbaI fragment into pART7 digested with Xhol/XbaI. Sequences consisting of the 35S promoter, the interrupted palindrome of PVY sequences and the OCS terminator were excised from pART7.PVY.LNYV.YVP as a 25 NotI fragment and cloned into pART27, a plasmid with the desired insert orientation was selected and designated pART27.PVY.LNYV.YVP.

**Plasmids pART7.35S.PVY.SCBV.YVP & pART27.35S.PVY.SCBV.YVP**

Plasmid pART7.35S.PVY.SCBV.YVP (Figure 65) was designed to co-express sense 30 and antisense constructs in transgenic plants. To generate this plasmid the PVY

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fragment from Cla pBC.PVY was cloned as a Xhol/EcoRI fragment into xhol/EcoRI-digested p35S.SCBV.O.SCBV.YVP. Sequences, consisting of the 35S promoter driving sense PVY sequences and the NOS terminator and the SCBV promoter driving antisense PVY and the OCS terminator were excised as a NotI fragment and cloned 5 into pART27, a plasmid with the desired insert orientation was isolated and designated pART27.35S.PVY.SCBV.YVP.

**Plasmids pART7.35S.PVYx3.SCBV.YVPx3 & pART27.35S.PVYx3.SCBV.YVPx3**

Plasmid pART7.35S.PVYx3.SCBV.YVPx3 (Figure 66) was designed to co-express 10 sense and antisense repeats of PVY in transgenic plants. to generate this plasmid, the intermediate pART7.35S.O.SCBV.YVPx3 was constructed by cloning the triple direct PVY repeat from ClapBC.PVYx3 as a Clal/Accl fragment into Cla-digested p35S.SCBV.cass and isolating a plasmid with an antisense orientation. for p35S.PVYx3.SCBV.YVPx3 the triple direct PVY repeat from Cla pBC.PVYx3 was 15 cloned as a KpnI/Smal fragment into KpnI/Smal-digested p35S.O.SCBV.YVPx3 to create p35S.PVYx3.SCBV.YVPx3. Sequences including both promoters, terminators and direct PVY repeats were isolated as a NotI fragment and cloned into pART27. A plasmid with an appropriate orientation was chosen and designated pART27.35S.PVYx3.SCBV.

20

**Plasmids pART7.PVYx3.LNYV.YVPx3 & pART27.PVYx3.LNYV.YVPx3**

Plasmid pART7.PVYx3.LNYV.YVPx3 (Figure 67) was designed to express triple repeats of PVY sequences as an interrupted palindrome. To generate this plasmid an intermediate, pART7x3.PVY.LNYV.YV was constructed by cloning a PVY.LNYV.YVP 25 fragment from pBC.PVY.LNYV.YVP as an Accl/Clal fragment into the plasmid pART7.PVYx2. pART7.35S.PVYx3.LNYV.YVPx3, was made by cloning an additional PVY direct repeat from pBC.PVYx2 as an Accl/Clal fragment into Clal digested pART7x3.PVY.LNYV.YVP. Sequences from pART7.35S.PVYx3.LNYV.YVPx3, including the 35S promoter, all PVY sequences and the OCS terminator were excised 30 as a NotI fragment and cloned into NotI-digested pART27, a plasmid with an

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appropriate orientation was chosen and designated pART27.35S.PVYx3.LNYV.

**Plasmids pART7.PVY multi & pART27.PVY multi**

Plasmid pART7.35S.PVY multi (Figure 68) was designed to express higher order direct  
5 repeats of regions of PVY sequences in transgenic plants. Higher order direct repeats  
of a 72 bp of the PVY Nia region from PVY were prepared by annealing two partially  
complementary oligonucleotides as follows:

PVY1:

10 5'-TAATGAGGATGATGTCCCTACCTTAATTGGCAGAAATTCTGTGGAAAGACAG  
GGAAATCTTCGGCATT-3'; and

PVY2:

5'-TTCTGCCAATTAAAGGTAGGGACATCATCCTCATTAAAATGCCGAAAGATT  
15 TCCCTGTCTTCCACAGAAAT-3'

The oligonucleotides were phosphorylated with T4 polynucleotide kinase, heated and  
cooled slowly to permit self-annealing, ligated with T4 DNA ligase, end-filled with  
Klenow polymerase and cloned into pCR2.1 (Invitrogen). Plasmids containing multiple  
20 repeats were isolated and sequences were cloned as EcoRI fragments in a sense  
orientation into EcoRI-digested pART7, to create the intermediate pART7.PVY multi.  
to create pART27.PVY multi, the 35S promoter, PVY sequences and the OCS  
terminator were excised as a NotI fragment and cloned into NotI-digested pART27.  
A plasmid with an appropriate insert orientation was isolated and designated  
25 pART27.PVY multi.

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## EXAMPLE 6

### Inactivation of virus gene expression in mammals

Viral immune lines are created by expressing viral sequences in stably transformed cell lines.

5

In particular, lytic viruses are used for this approach since cell lysis provides very simple screens and also offer the ability to directly select for potentially rare transformation events which might create viral immunity. Sub-genomic fragments derived from a simple single stranded RNA virus (Bovine enterovirus - BEV) or a 10 complex double stranded DNA virus, Herpes Simplex Virus I (HSV I) are cloned into a suitable vector and expressed in transformed cells. Mammalian cell lines are transformed with genetic constructs designed to express viral sequences driven by the strong cytomegalovirus (CMV-IE) promoter. Sequences utilised include specific viral replicase genes. Random "shotgun" libraries comprising representative viral gene 15 sequences, may also be used and the introduced dispersed nucleic acid molecule, to target the expression of virus sequences.

Exemplary genetic constructs for use in this procedure, comprising nucleotide sequences derived from the BEV RNA-dependent RNA polymerase gene, are 20 presented herein.

For viral polymerase constructs, large numbers (approximately 100) of transformed cell lines are generated and infected with the respective virus. For cells transformed with shotgun libraries very large numbers (hundreds) of transformed lines are generated 25 and screened in bulk for viral immunity. Following virus challenge, resistant cell lines are selected and analysed further to determine the sequences conferring immunity thereon.

Resistant cell lines are supportive of the ability of the introduced nucleotide sequences 30 to inactivate viral gene expression in a mammalian system.

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Additionally, resistant lines obtained from such experiments are used to more precisely define molecular and biochemical characteristics of the modulation which is observed.

5

## EXAMPLE 8

### Induction of virus resistance in transgenic plants

*Agrobacterium tumefaciens*, strain LBA4404, was transformed independently with the constructs pART27.PVY, pART27.PVYx2, pART27.PVYx3, pART27.PVYx4, pART27.PVY.LNYV.PVY, pART27.PVY.LNYV.YVP<sub>A</sub>, pART27.PVY.LNYV.YVP, 10 pART27.35S.PVY.SCBV.O, pART27.35S.O.SCBV.PVY, pART27.35S.O.SCBV.YVP, pART27.35S.PVY.SCBV.YVP, pART27.35S.PVYx3.SCBV.YPVx3, pART27.PVYx3.LNYV.YVPx3 and pART27.PVYx10, using tri-parental matings. DNA mini-preps from these strains were prepared and examined by restriction with NotI to ensure they contained the appropriate binary vectors.

15

*Nicotiana tabaccum* (cultivar W38) were transformed with these *Agrobacterium* strains using standard procedures. Putative transformed shoots were excised and rooted on media containing kanamycin. Under these conditions we have consistently observed that only transgenic shoots will root on kanamycin plates. Rooted shoots were 20 transferred to soil and allowed to establish. After two to three weeks, vigorous plants with at least three sets of leaves were chosen and infected with PVY.

Viral inoculum was prepared from W38 tobacco previously infected with the virus, approximately 2 g of leaf material, showing obvious viral symptoms were ground with 25 carbarundum in 10 ml of 100mM Na phosphate buffer (pH 7.5). the inoculum was diluted to 200 ml with additional Na phosphate buffer. Two leaves from each transgenic plant were sprinkled with carbarundum, then 0.4 ml of inoculum was applied to each leaf and leaves rubbed fairly vigorously with fingers. Using this procedure 100% of non-transgenic control plants were infected with PVY.

30

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To assay for viral resistance and immunity transgenic plants are monitored for symptom development. The PVY strain (PVY-D, an Australian PVY isolate) gives obvious symptoms on W38 tobacco, a vein clearing symptom is readily observed on the two leaves above the inoculated leaves, subsequent leaves show uniform chlorotic 5 lesions. Symptom development was monitored over a six week period.

Transgenic lines were described as resistant if they showed reduced viral symptoms, which manifests as a reduction in the leaf area showing chlorotic lesions. Resistance ranges from very strong resistance where only a few viral lesions are observed on a 10 plant to weak resistance which manifests as reduced symptoms on leaves that develop late in plant growth.

Transgenic plants which showed absolutely no evidence of viral symptoms were classified as immune. To ensure these plants were immune they were re-inoculated 15 with virus, most plants remained immune, the few that showed symptoms were re-classified as resistant.

For plant lines generated Southern blots are performed, resistance in subsequent generations is monitored to determine that resistance/immunity is transmissible. 20 Additionally, the breadth of viral resistance is monitored by challenging lines with other PVY strains, to determine whether host range susceptibility is modified.

Results from these experiments are described in Table 2 . These data indicate that constructs comprising tandem repeats of target gene sequence, either in the 25 configuration of palindromes, interrupted palindromes as direct repeat sequences, are capable of conferring viral resistance and/or immunity in transgenic plants.

Accordingly, such inverted and/or direct repeat sequences modulate expression of the virus target gene in the transgenic plant.

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Constructs combining the use of direct and inverted repeat sequences, namely pART27.35S.PVYx3.SCBV.YVPx3 and pART27.PVYx3.LNYV.YVPx3, are also useful in modulating gene expression.

5

### EXAMPLE 9

#### Inactivation of Galt in animal cells

To assay for Galt inactivation, porcine PK2 cells were transformed with the relevant constructs. PK2 cells constitutively express Galt enzyme, the activity of which results in the addition of a variety of  $\alpha$ -1,3-galactosyl groups to a range of proteins expressed 10 on the cell surface of these cells. Cells were transformed using lipofectin and stably transformed lines were selected using genetecin.

As an initial assay cell lines were probed for the presence of the Galt-encoded epitope, i.e.  $\alpha$ -1,3-galactosyl moieties decorating cell surface proteins, using the lectin IB4. IB4 15 binding was assayed either *in situ* or by FACS sorting.

For *in situ* binding, cells were fixed to solid supports with cold methanol for 5 mins, cells were rinsed in PBS (phosphate buffered saline) and non-specific IB4 binding was blocked with 1% BSA in PBS for 10 mins. Fixed cells were probed using 20 ug/ml IB4- 20 biotin (Sigma) in 1% BSA, PBS for 30 mins at room temperature, cells were washed in PBS then probed with a 1:200 dilution of ExtrAvidin-FITC (Sigma) in PBS for 30 mins followed by further rinses in PBS. Cells were then examined using fluorescence microscopy, under these conditions the outer surface of PK2 control cells uniformly stained green.

25

For FACS analysis, cells were suspended after treatment with trypsin, washed in HBSS/Hepes (Hank's buffered saline solution with 20 mM Hepes, pH7.4) and probed with 10 ug/ml IB4-biotin (Sigma) in HBSS/Hepes for 45 mins at 4°C. Cells were washed in HBSS/Hepes, probed with a 1:200 dilution of ExtrAvidin-FITC (Sigma) in 30 HBSS/Hepes for 45 mins at 4°C and rinsed in cold HBSS/Hepes prior to FACS

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sorting.

Using this approach transformed cell lines are assayed for Galt inactivation and quantitative assessment of construct effectiveness is determined. Moreover cell lines  
5 showing Galt inactivation are isolated and subject to further molecular analyses to determine the mechanism of gene inactivation.

PLASMID CONSTRUCT	No. OF PLANTS TESTED	PERCENTAGE OF PLANTS SHOWING SPECIFIED PHENOTYPE		
		SUSCEPTIBLE	IMMUNE	RESISTANT
pART27.PVV	19	16	1	2
pART27.PVVx2	13	5	4	4
pART27.PVVx3	21	2	5	14
5 pART27.PVVx4	21	5	7	9
pART27.35S.PVV.SCBC.0	25	8	0	17
pART27.35S.O.SCBB.PVV	22	8	0	14
pART27.35S.O.SCBB.VV <sub>P</sub>	18	14	0	4
10 pART27.35S.PVV.SCBB.VV <sub>P</sub>	17	3	8	6
pART27.PVV.LNYY.PVV	26	18	2	6
pART27.PVV.LNYY.VV <sub>P</sub>	20	6	10	4
pART27.PVV.LNYY.VV <sub>P4</sub>	18	7	11	0

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**CLAIMS**

1. A method of repressing, delaying or otherwise reducing the expression of a target gene in a cell, tissue or organ, said method comprising introducing to said cell, tissue or organ one or more dispersed nucleic acid molecules or foreign nucleic acid molecules comprising multiple copies of a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a region thereof or complementary thereto for a time and under conditions sufficient for translation of the mRNA product of said target gene to be modified, subject to the proviso that the transcription of said mRNA product is not exclusively repressed or reduced.  
10
2. The method according to claim 1 wherein the dispersed nucleic acid molecules or foreign nucleic acid molecules comprise inverted repeats of the target gene sequence or a region thereof or complementary thereto.
- 15 3. The method according to claim 1 wherein the dispersed nucleic acid molecules or foreign nucleic acid molecules comprise direct repeats of the target gene sequence or a region thereof or complementary thereto.
4. The method according to claim 1 wherein the dispersed nucleic acid molecules or foreign nucleic acid molecules comprise both direct and inverted repeats of the target gene sequence or a region thereof or complementary thereto.  
20
5. The method according to any one of claims 1 to 4, wherein the number of copies of the target gene sequence or region thereof or complementary thereto in the dispersed nucleic acid molecule or foreign nucleic acid molecule is two.  
25
6. The method according to any one of claims 1 to 4, wherein the number of copies of the target gene sequence or region thereof or complementary thereto in the dispersed nucleic acid molecule or foreign nucleic acid molecule is three.

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7. The method according to any one of claims 1 to 4, wherein the number of copies of the target gene sequence or region thereof or complementary thereto in the dispersed nucleic acid molecule or foreign nucleic acid molecule is four.
- 5 8. The method according to any one of claims 1 to 4, wherein the number of copies of the target gene sequence or region thereof or complementary thereto in the dispersed nucleic acid molecule or foreign nucleic acid molecule is six.
9. The method according to any one of claims 1 to 4, wherein the number of 10 copies of the target gene sequence or region thereof or complementary thereto in the dispersed nucleic acid molecule or foreign nucleic acid molecule is ten.
10. The method according to any one of claims one to 9 wherein the dispersed nucleic acid molecule or foreign nucleic acid molecule comprises tandem repeats of 15 the target gene sequence and wherein one or more of the repeated units of said tandem repeats is separated from another unit by a nucleic acid-containing stuffer fragment.
11. The method according to any one of claims 1 to 10 wherein the cell, tissue or 20 organ is an animal cell, tissue or organ.
12. The method according to claim 11 wherein the animal is a mouse.
13. The method according to any one of claims 1 to 10 wherein the cell, tissue or 25 organ is a plant cell, tissue or organ.
14. The method according to claim 13 wherein the plant is a tobacco plant.
15. The method according to any one of claims 1 to 14 wherein the target gene is 30 a gene which is contained within the genome of the cell, tissue or organ.

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16. The method according to claim 15 wherein the target gene is  $\alpha$ -1,3-galactosyltransferase.

17. The method according to any one of claims 1 to 14 wherein the target gene is  
5 derived from the genome of a pathogen of the cell, tissue or organ or an organism  
comprising said cell, tissue or organ.

18. The method according to claim 17 wherein the pathogen is a virus.

10 19. The method according to claim 18 wherein the virus is an animal pathogen.

20. The method according to claim 19 wherein the virus is BEV.

21. The method according to claim 18 wherein the virus is a plant pathogen.

15

22. The method according to claim 21 wherein the virus is PVY.

23. The method according to any one of claims 1 to 22 further comprising selecting  
the dispersed nucleic acid molecule(s) or foreign nucleic acid molecule(s) according  
20 to their ability to effectively modulate expression of the target gene.

24. A method of repressing, delaying or otherwise reducing the expression of a  
target gene in a cell, tissue or organ, said method comprising:

- (i) selecting one or more dispersed nucleic acid molecules or foreign nucleic  
acid molecules which comprise tandem repeats of a nucleotide sequence which  
is substantially identical to the nucleotide sequence of said target gene or a  
region thereof or which is complementary thereto;
- (ii) producing a synthetic gene comprising said dispersed nucleic acid  
molecules or foreign nucleic acid molecules operably connected to a promoter  
30 sequence operable in said cell, tissue or organ;

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- (iii) introducing said synthetic gene to said cell, tissue or organ; and  
(iv) expressing said synthetic gene in said cell, tissue or organ for a time and under conditions sufficient for translation of the mRNA product of said target gene to be modified, subject to the proviso that the transcription of said mRNA product is not exclusively repressed or reduced.

25. A method of conferring resistance or immunity to a viral pathogen upon a cell, tissue, organ or whole organism, comprising introducing one or more dispersed nucleic acid molecules or foreign nucleic acid molecules which comprise tandem repeats of  
10 a nucleotide sequence derived from the viral pathogen or a complementary sequence thereto for a time and under conditions sufficient for translation of the mRNA product of a virus gene to be delayed or otherwise reduced, subject to the proviso that the transcription of said mRNA product is not exclusively repressed or reduced.

15 26. The method according to claim 25 wherein the viral pathogen is a plant  
pathogen.

27. The method according to claim 26 wherein the virus is PVY

20 28. The method according to claim 25 wherein the virus is an animal pathogen

29. The method according to claim 28 wherein the virus is BEV

30. The method according to any one of claims 25 to 29 further comprising selecting  
25 the dispersed nucleic acid molecule(s) or foreign nucleic acid molecule(s) according  
to their ability to confer resistance or immunity on the cell, tissue, organ or organism.

31. A method of conferring resistance or immunity to a viral pathogen upon a cell, tissue, organ or whole organism, comprising:

30 (i) selecting one or more dispersed nucleic acid molecules or foreign nucleic

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acid molecules which comprise tandem repeats of a nucleotide sequence derived from the viral pathogen or a complementary sequence thereto;

5 (ii) producing a synthetic gene comprising said dispersed nucleic acid molecules or foreign nucleic acid molecules operably connected to a promoter sequence operable in said cell, tissue, organ or whole organism;

(iii) introducing said synthetic gene to said cell, tissue, organ or whole organism; and

(iv) expressing said synthetic gene in said cell, tissue or organ for a time and under conditions sufficient for translation of the mRNA product of a gene of the 10 virus to be modified, subject to the proviso that the transcription of said mRNA product is not exclusively repressed or reduced.

32. The method according to any one of claims 25 to 31, wherein the dispersed nucleic acid molecules or foreign nucleic acid molecules comprise multiple copies of 15 nucleotide sequence encoding a viral replicase, polymerase, coat protein or uncoating gene.

33. The method according to claim 32 wherein the dispersed nucleic acid molecules or foreign nucleic acid molecules comprise multiple copies of nucleotide sequence 20 encoding a viral polymerase.

34. The method according to claim 32 wherein the dispersed nucleic acid molecules or foreign nucleic acid molecules comprise multiple copies of nucleotide sequence encoding a viral coat protein.

25

35. A synthetic gene which is capable of repressing, delaying or otherwise reducing the expression of a target gene in a cell, tissue, organ or whole organism, wherein said synthetic gene comprises a dispersed nucleic acid molecule or a foreign nucleic acid molecule comprising multiple copies of a nucleotide sequence which is substantially 30 identical to the nucleotide sequence of said target gene or a derivative thereof or a

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complementary sequence thereto placed operably under the control of a promoter sequence which is operable in said cell, tissue, organ or whole organism.

36. The synthetic gene according to claim 35, wherein the dispersed nucleic acid  
5 molecule or a foreign nucleic acid molecule comprises tandem inverted and/or direct repeats of a genetic sequence that is endogenous to the genome of the cell, tissue, organ or organism or which is derived from a non-endogenous gene of the cell, tissue, organ or organism.

10 37. The synthetic gene according to claim 36 wherein the non-endogenous gene is derived from a viral pathogen of the cell, tissue, organ or organism.

38. The synthetic gene according to claim 37 wherein the non-endogenous gene is derived from an animal virus.

15

39. The synthetic gene according to claim 38 wherein the animal virus is BEV.

40. The synthetic gene according to claim 38 wherein the non-endogenous gene is derived from the BEV polymerase gene.

20

41. The synthetic gene according to claim 40 wherein the promoter is the CMV-IE promoter or SV40 promoter sequence.

25 42. The synthetic gene according to claim 37 wherein the non-endogenous gene is derived from a plant virus.

43. The synthetic gene according to claim 42 wherein the plant virus is PVY.

30 44. The synthetic gene according to claim 43 wherein the promoter is the CaMV 35S promoter or the SCBV promoter sequence.

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45. The synthetic gene according to claims 35 or 36 wherein the dispersed nucleic acid molecule or a foreign nucleic acid molecule comprises tandem inverted and/or direct repeats of the porcine  $\alpha$ -1,3-galactosyltransferase gene.

5 46. The synthetic gene according to claim 45 wherein the porcine  $\alpha$ -1,3-galactosyltransferase gene is placed operably in connection with the CMV promoter sequence.

10 47. The synthetic gene according to any one of claims 35 to 46 wherein the multiple copies of the nucleotide sequence of the target gene are operably connected to two or more promoter sequences.

15 48. The synthetic gene according to claim 47 wherein each of the multiple copies of the nucleotide sequence of the target gene are operably connected to spatially separate promoter sequences.

49. A genetic construct comprising the synthetic gene according to any one of claims 35 to 48.

20 50. The genetic construct according to claim 49 selected from the list comprising plasmid pCMV.BEVx2; plasmid pCMV.BEV.GFP.VEB; plasmid pCMV.BEV.SV40L.BEV; and plasmid pCMV.BEV.SV40L.VEB.

51. The genetic construct according to claim 49 selected from plasmid 25 pCMV.Galtx2; and pCMV.Galtx4.

52. The genetic construct according to claim 49 selected from the list comprising plasmid pSP72.PVYx2; plasmid pBC.PVYx2; plasmid pBC.PVYx3; plasmid pBC.PVYx4; plasmid pART27.PVYx2; plasmid pART27.PVYx3; plasmid 30 pART27.PVYx4; plasmid pBC.PVY.LNYV.YVP $\Delta$ ; plasmid pBC.PVY.LNYV.YVP;

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plasmid pBC.PVY.LNYV.PVY; plasmid pART27.PVY.LNYV.PVY; plasmid pART27.PVY.LNYV.YVP<sub>Δ</sub>; plasmid pART27.PVY.LNYV.YVP; plasmid pART27.35S.PVY.SCBV.YVP; plasmid pART27.35S.PVYx3.SCBV.YVPx3; plasmid pART27.PVYx3.LNYV.YVPx3; and plasmid pART27.PVYx10.

5

53. Use of the genetic construct according to claim 50 to confer immunity or resistance against BEV upon an animal cell, tissue or organ or a whole animal.

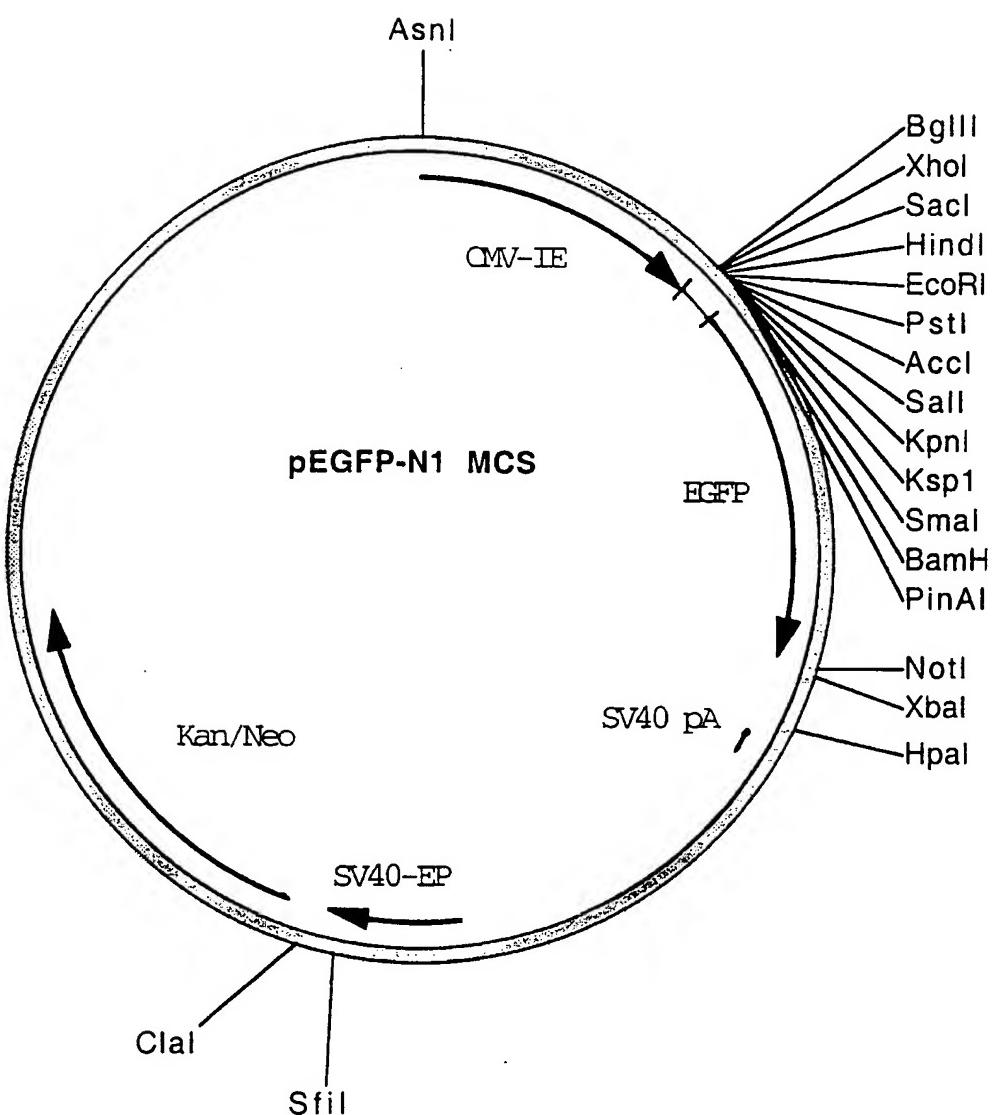
54. Use of the genetic construct according to claim 51 to delay, repress or otherwise  
10 reduce expression of α-1,3-galactosyltransferase in a cell, tissue, organ or whole  
organism that would otherwise express same.

55. Use of the genetic construct according to claim 52 to confer immunity or  
resistance against PVY upon a plant cell, tissue, organ or whole plant.

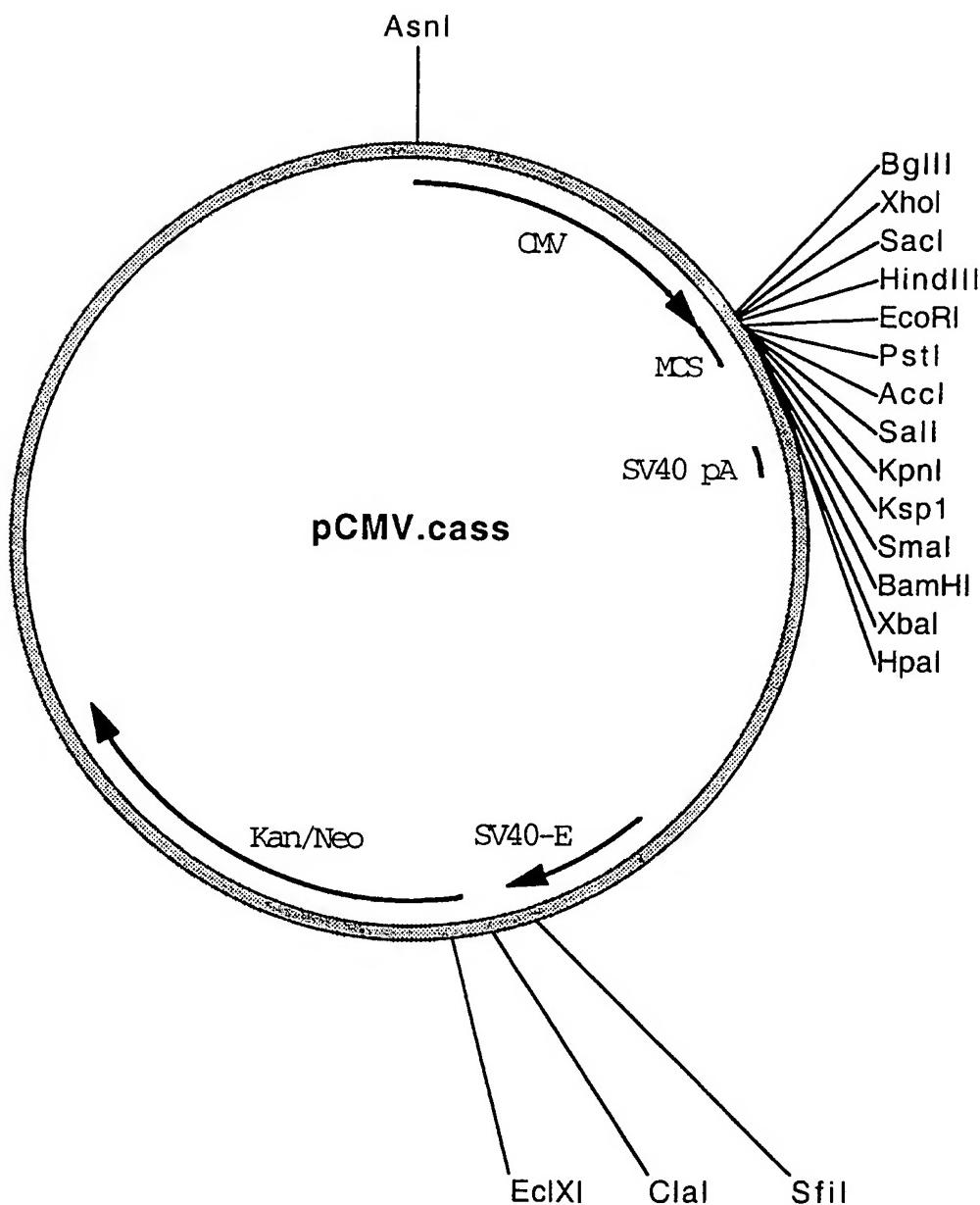
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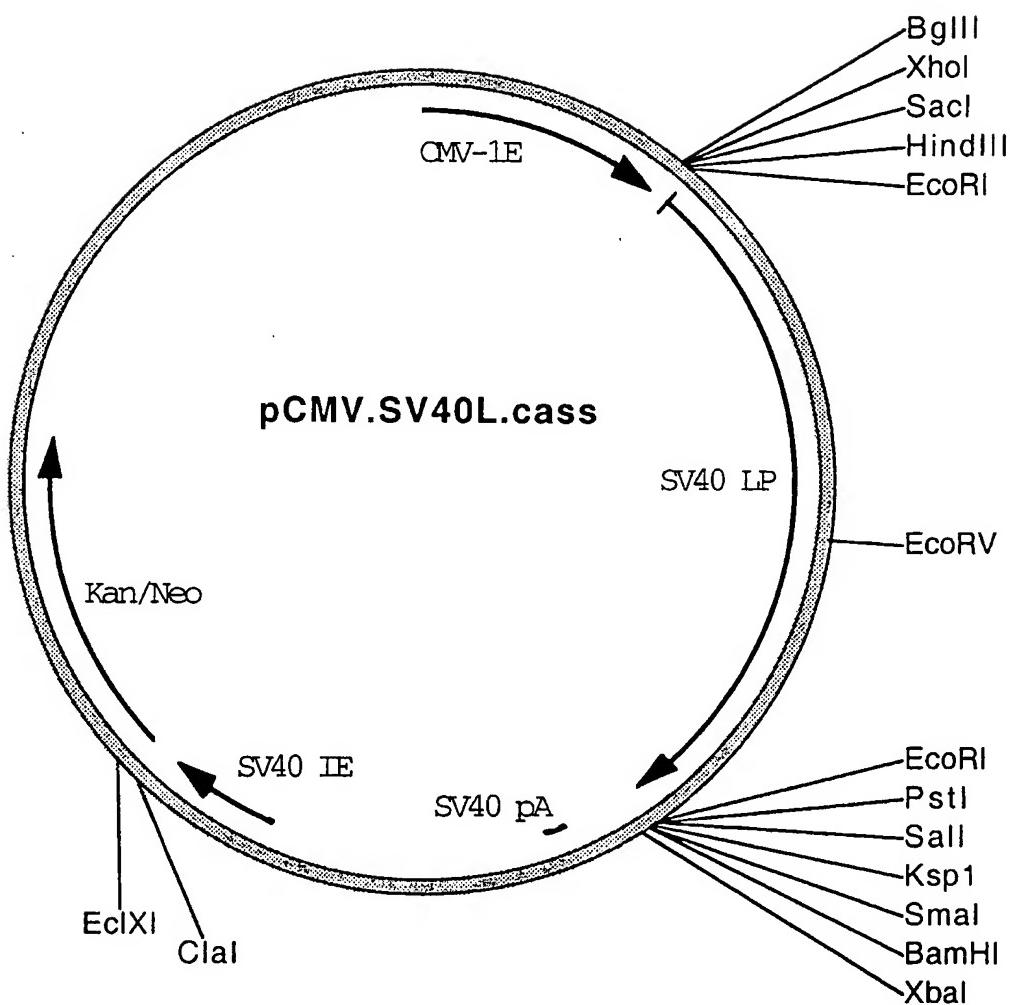
56. Use according to claim 55, wherein the plant is tobacco.

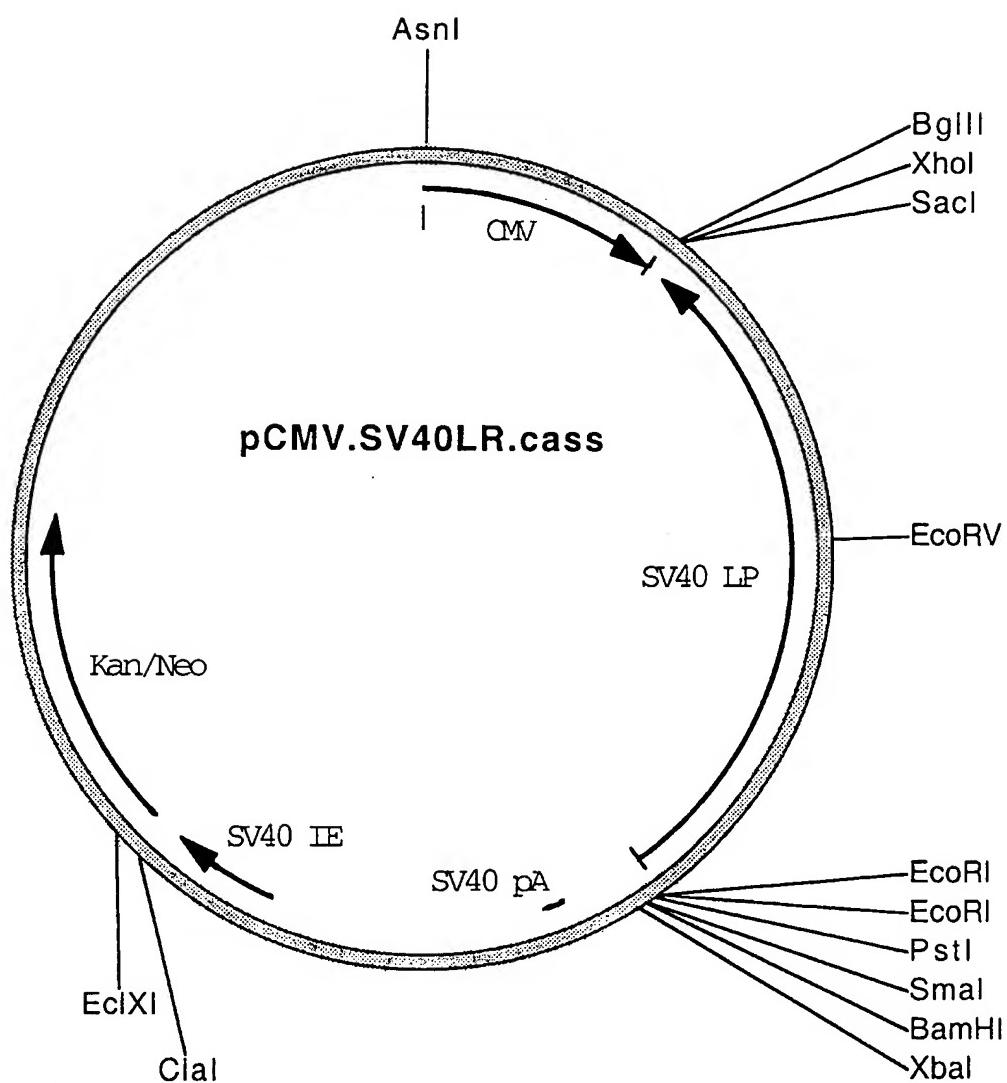
57. A cell, tissue, organ or whole organism comprising the synthetic gene according  
to any one of claims 35 to 48 or the genetic construct according to any one of claims  
20 49 to 52 .

**FIGURE 1**

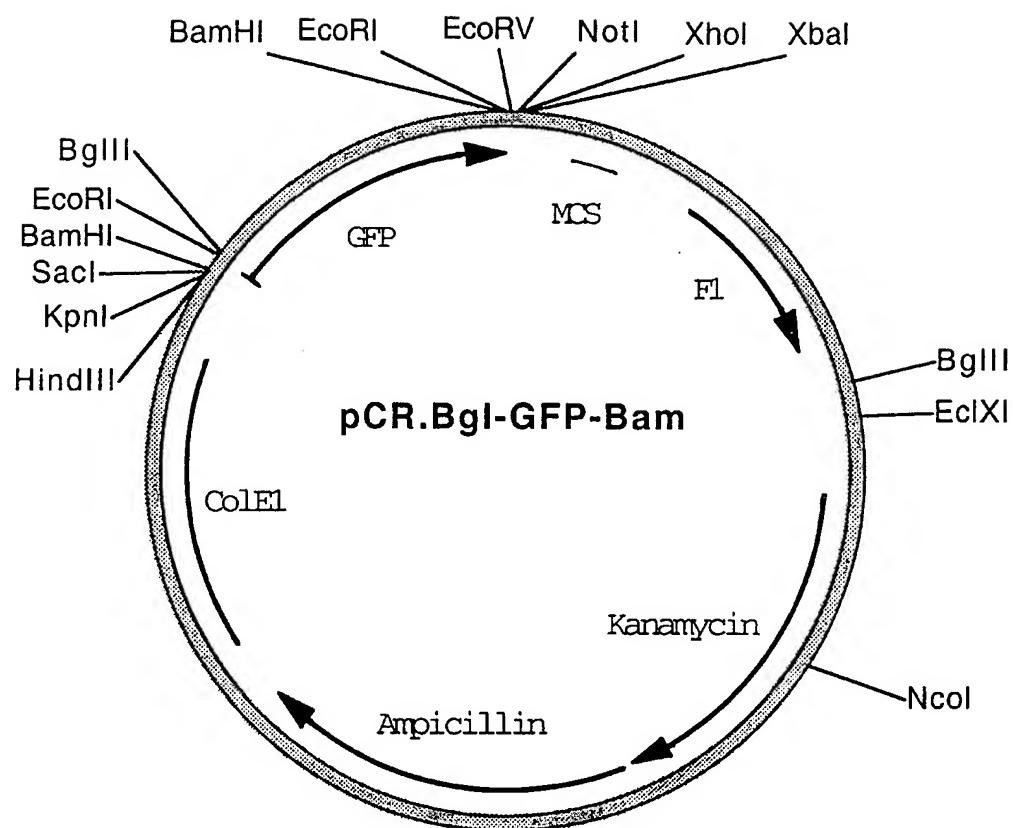
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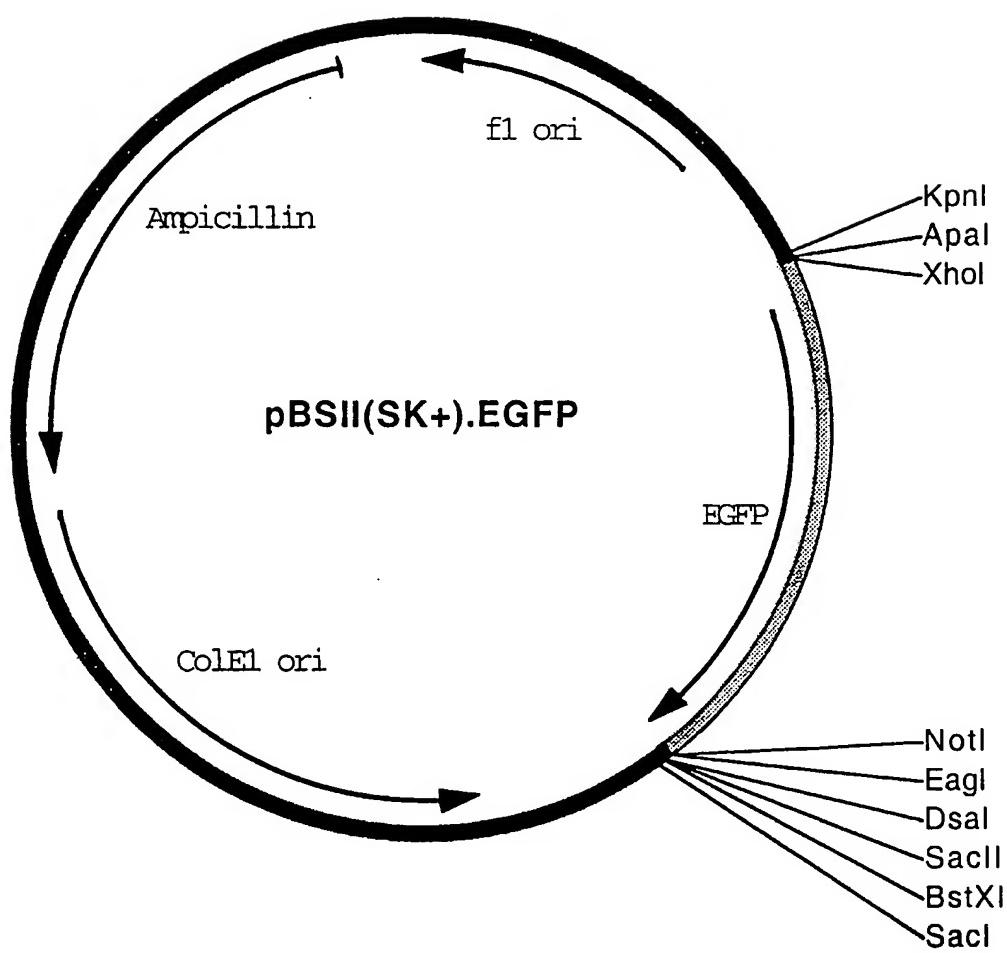
**FIGURE 2**

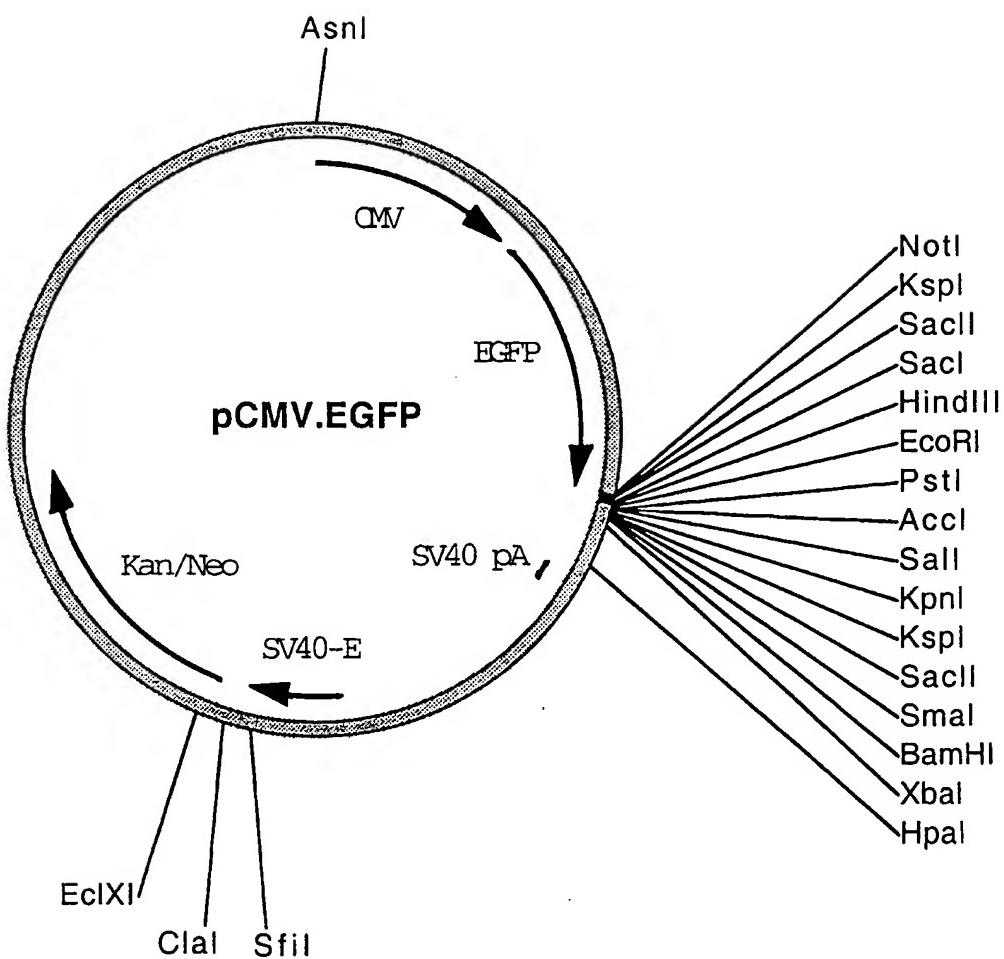
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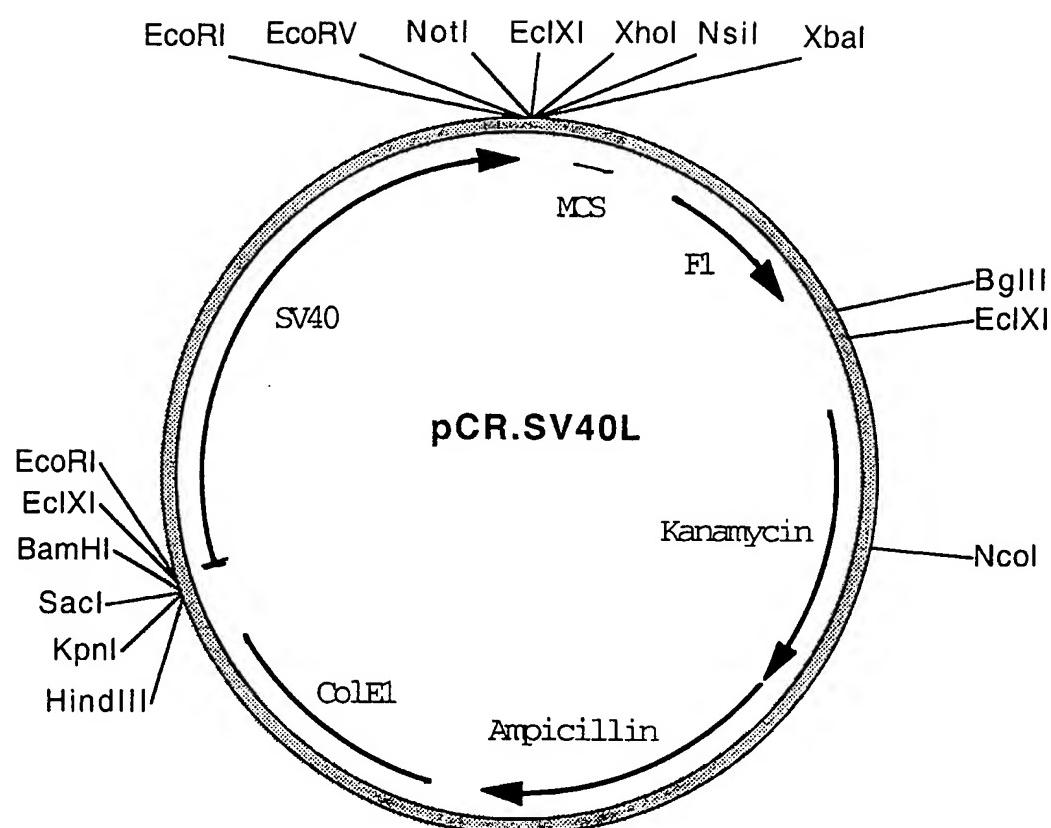
**FIGURE 4**

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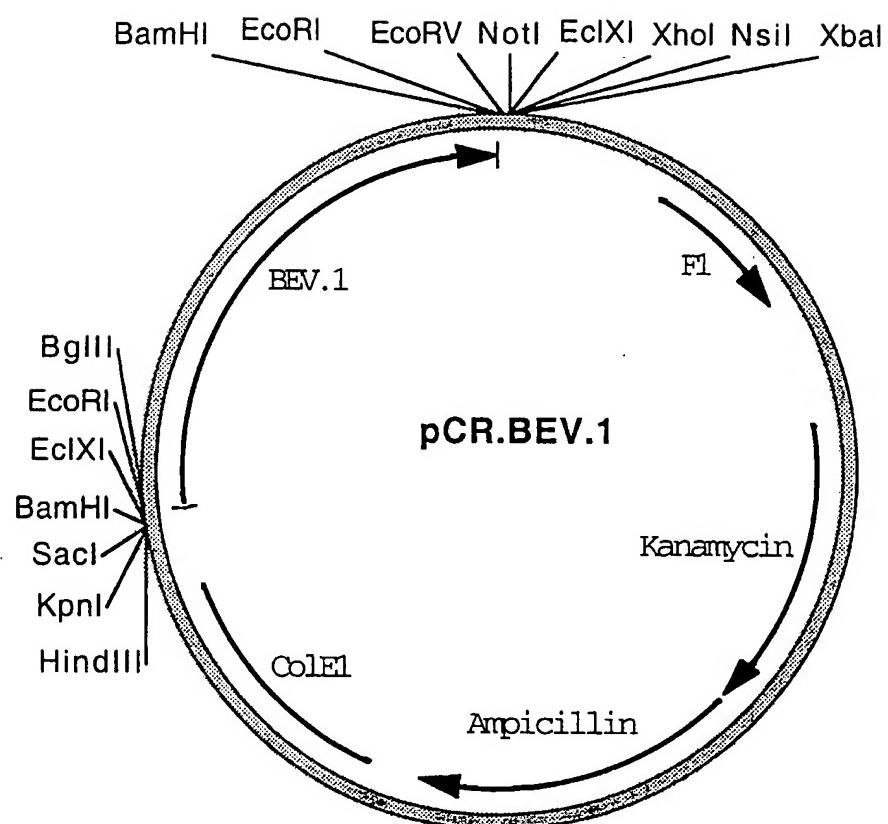
**FIGURE 5**

**FIGURE 6**

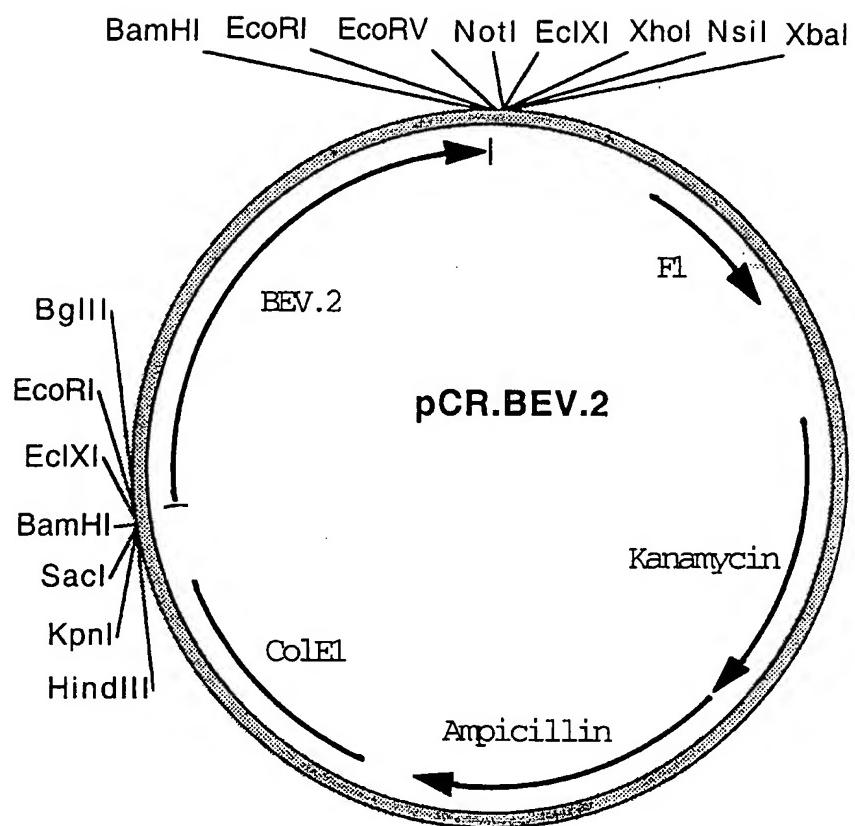
**FIGURE 7**

**FIGURE 8**

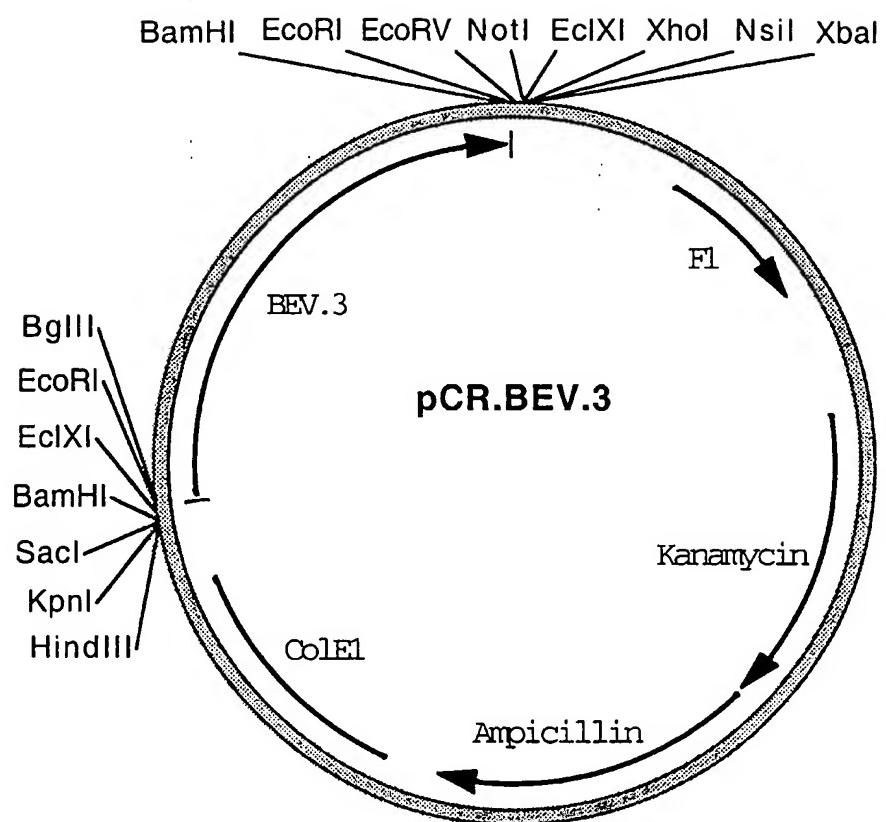
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**FIGURE 9**

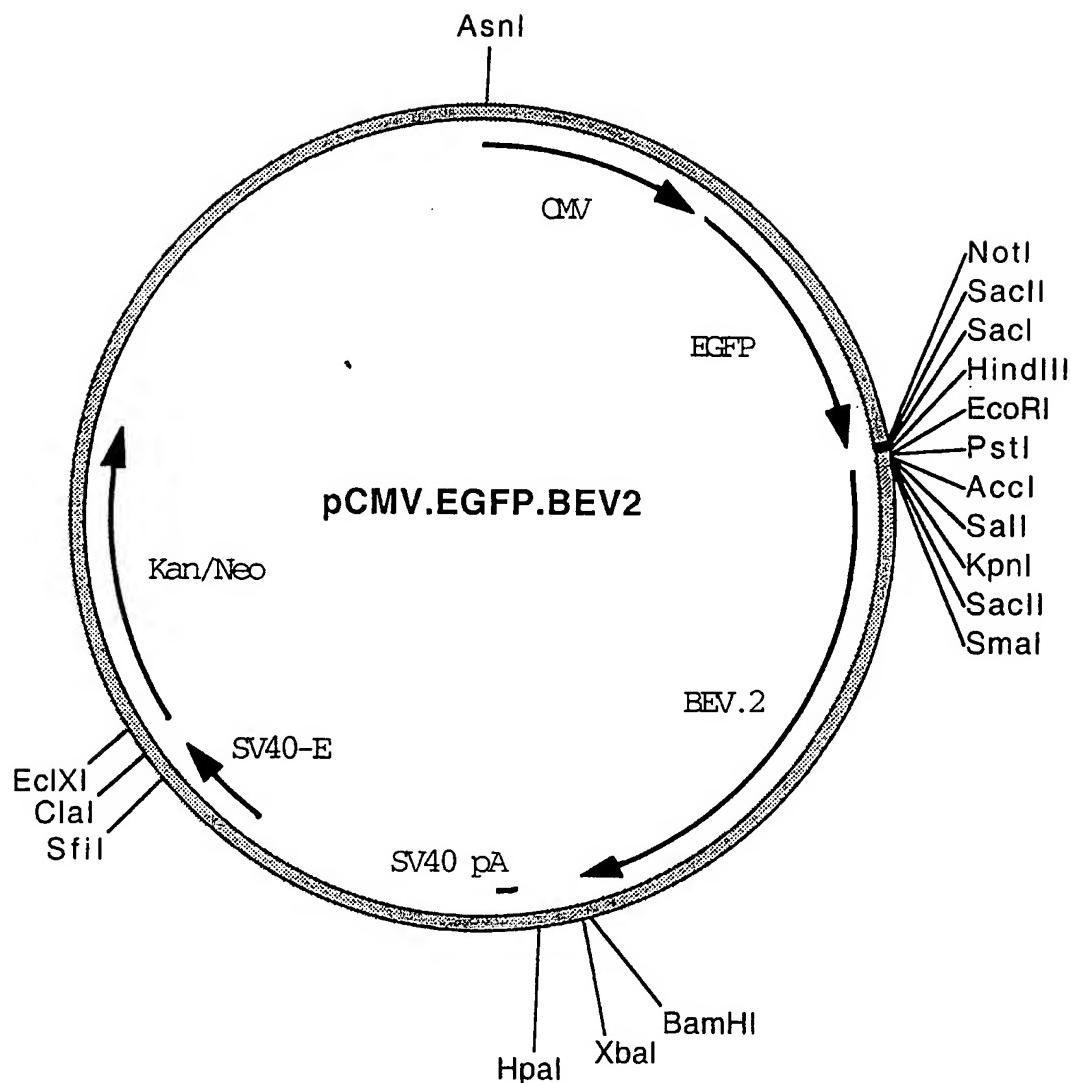
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**FIGURE 10**

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**FIGURE 11**

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**FIGURE 12**

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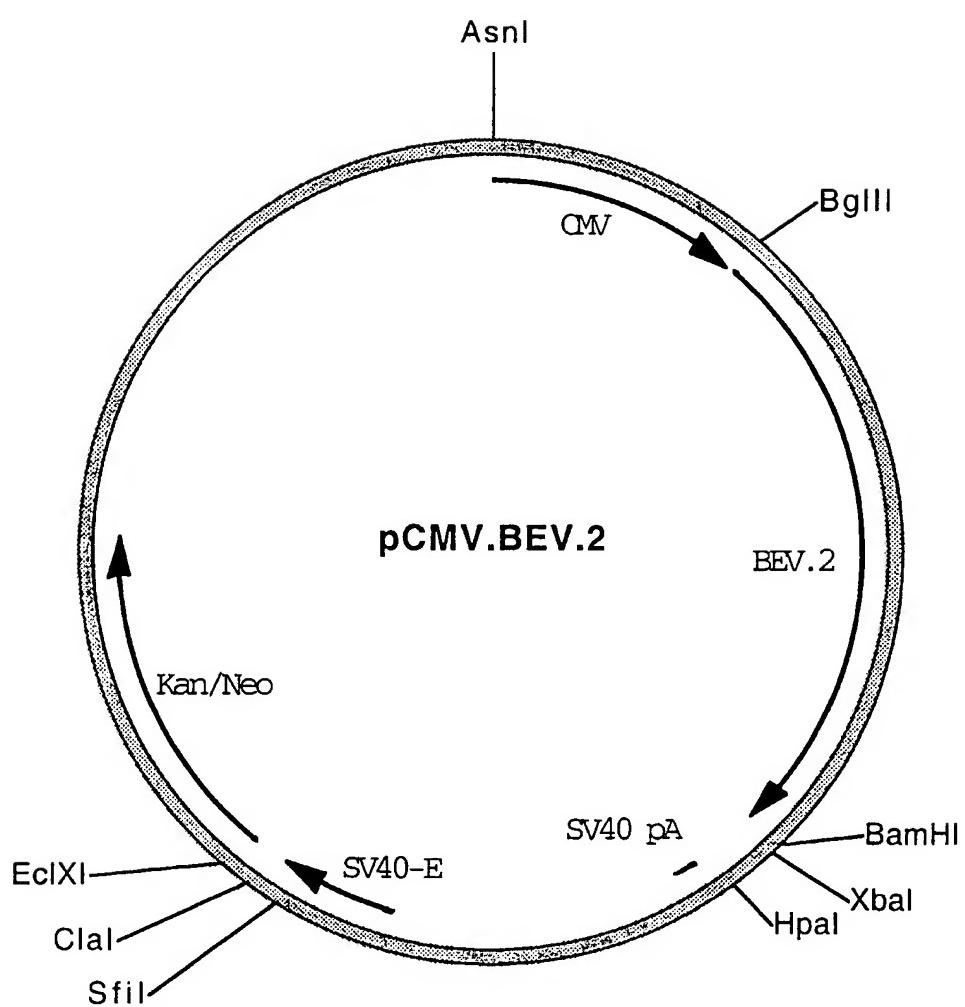
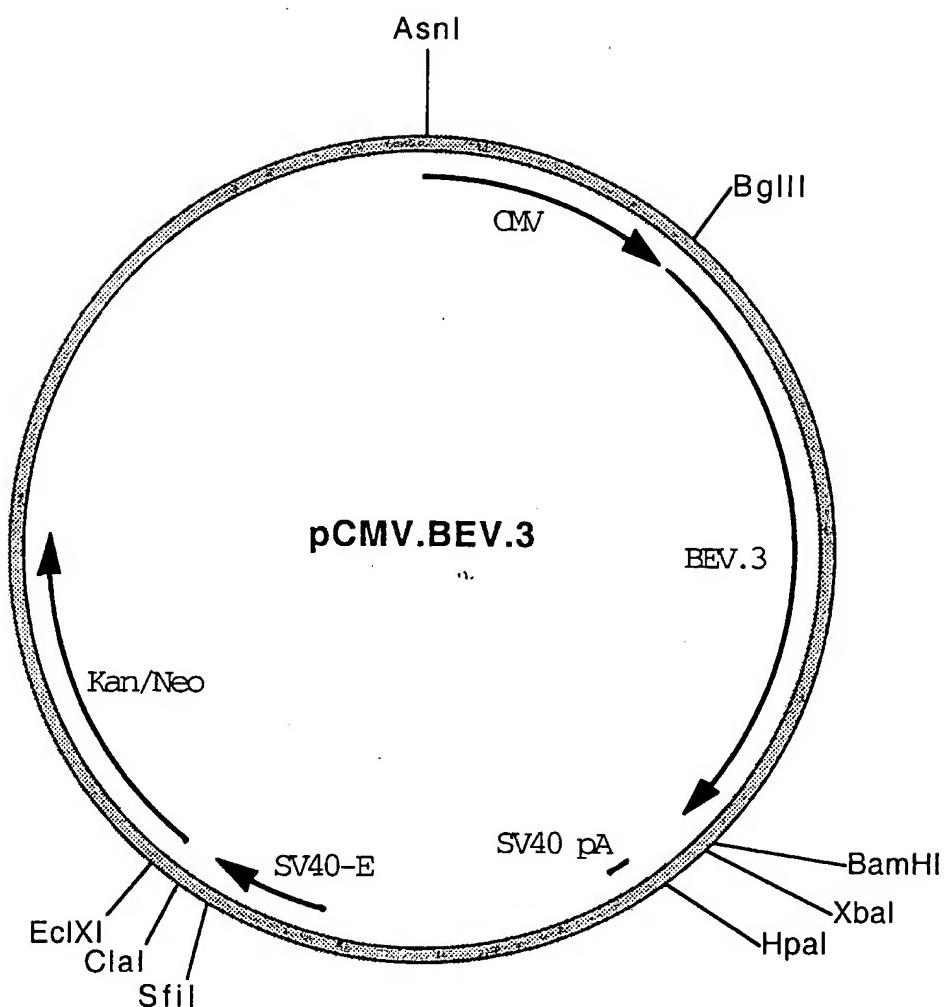
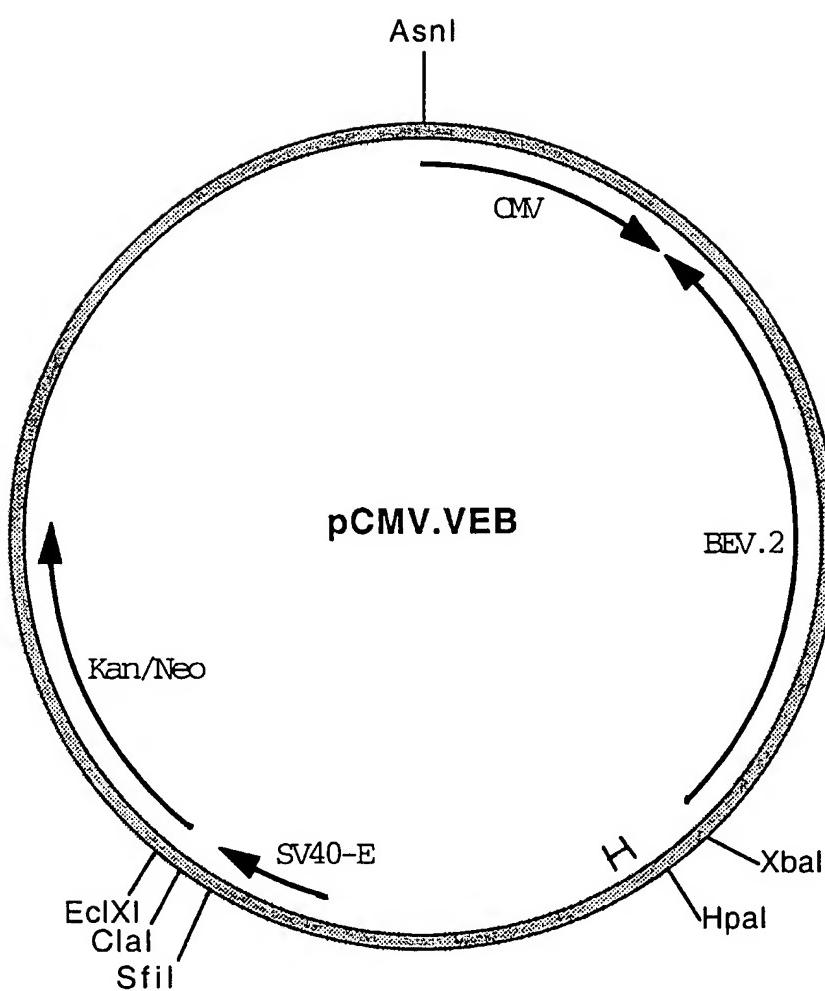


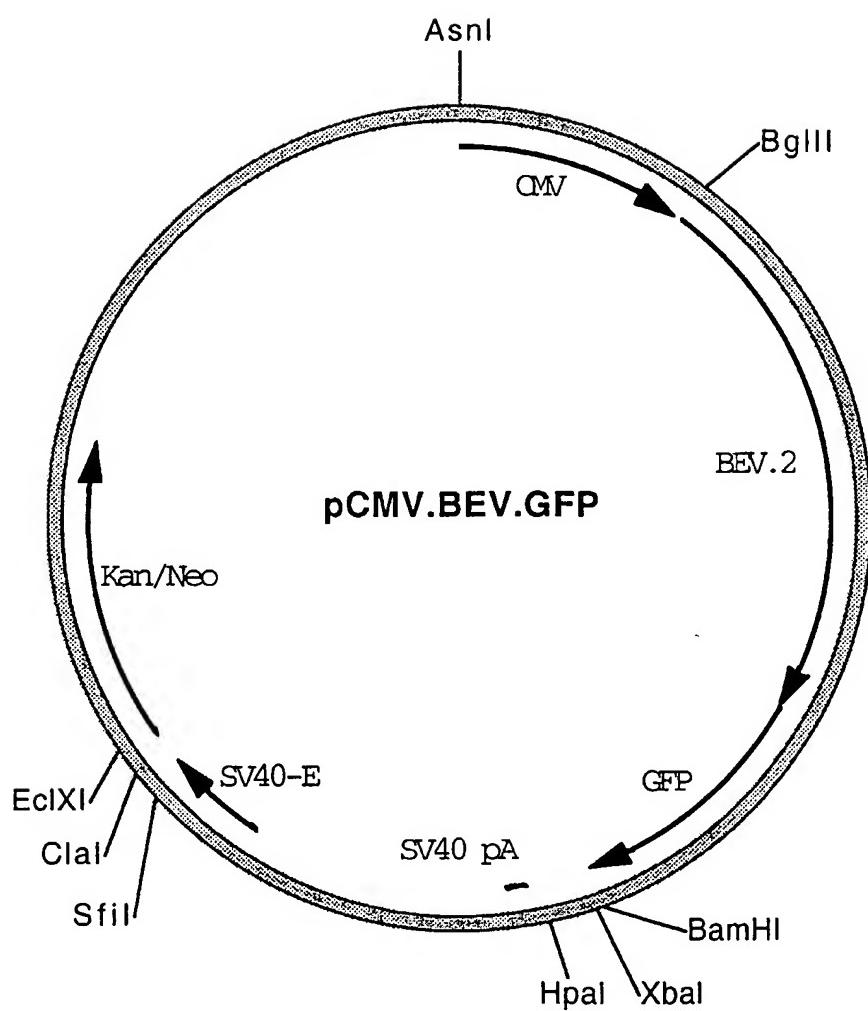
FIGURE 13

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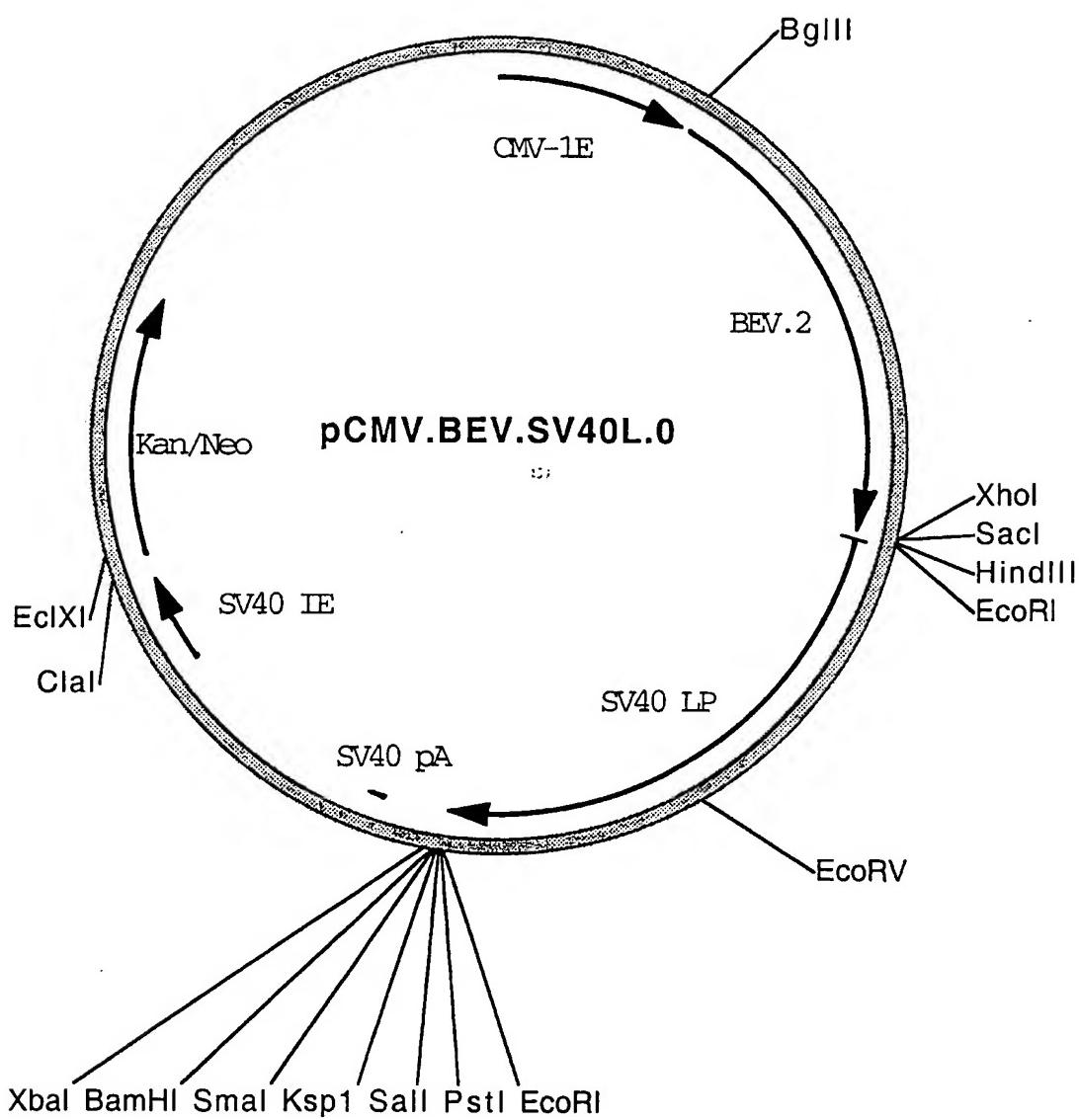
**FIGURE 14**

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**FIGURE 15**

**FIGURE 16**

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**FIGURE 17**

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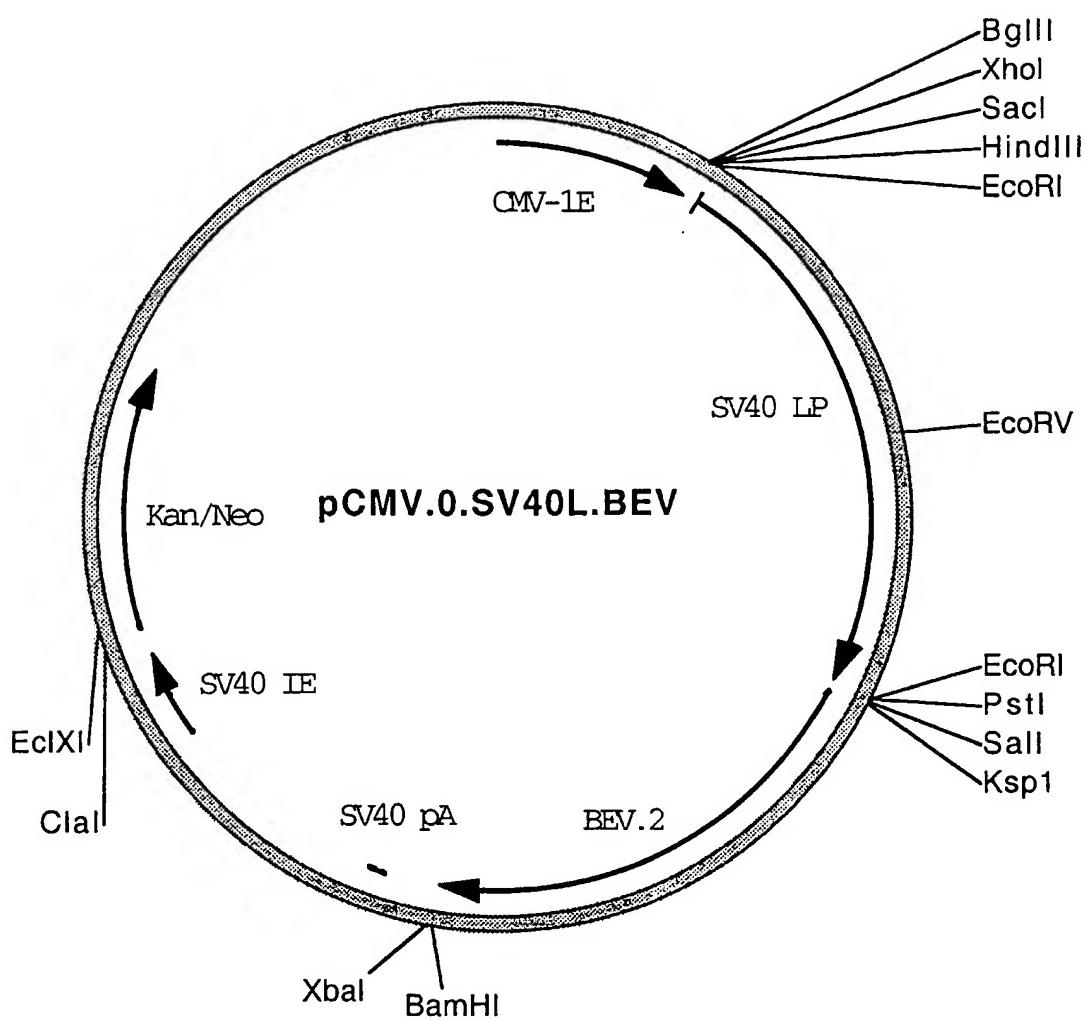
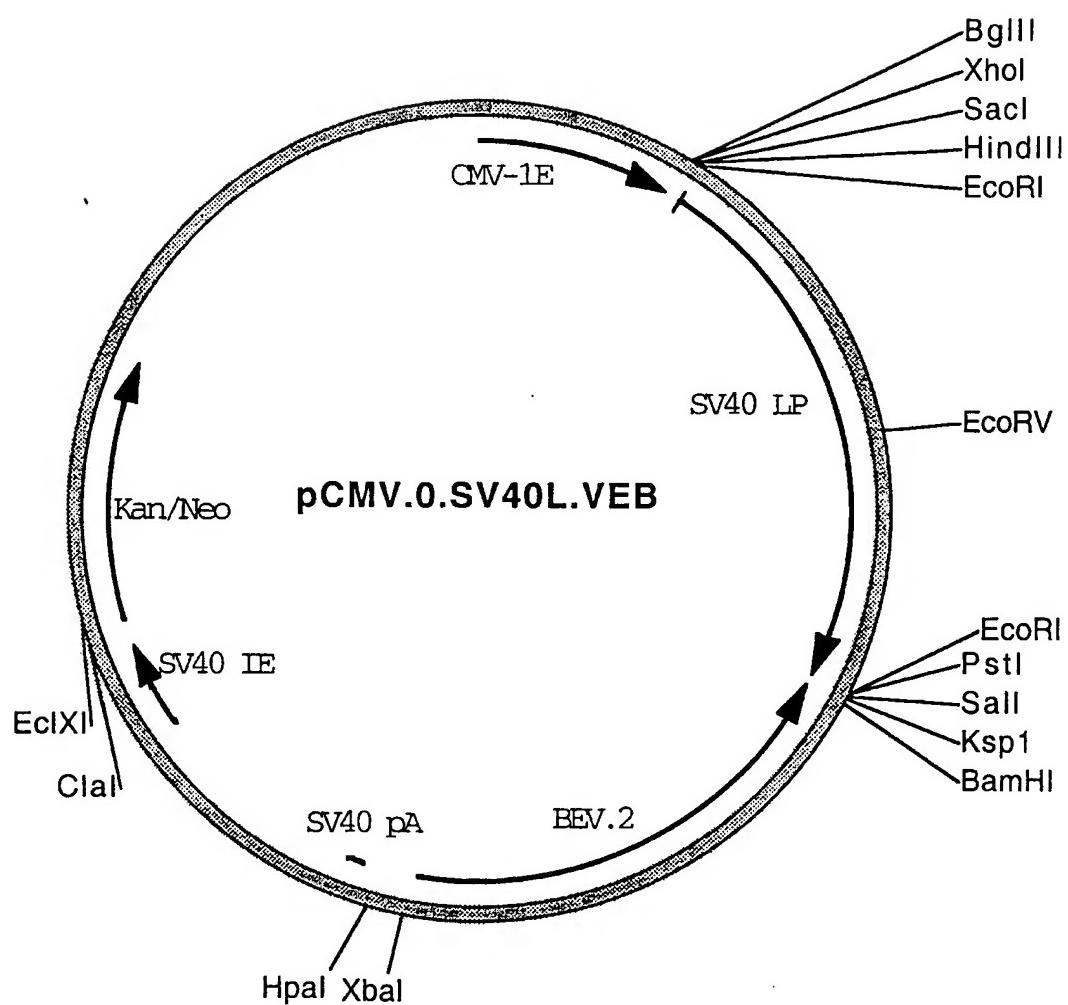


FIGURE 18

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**FIGURE 19**

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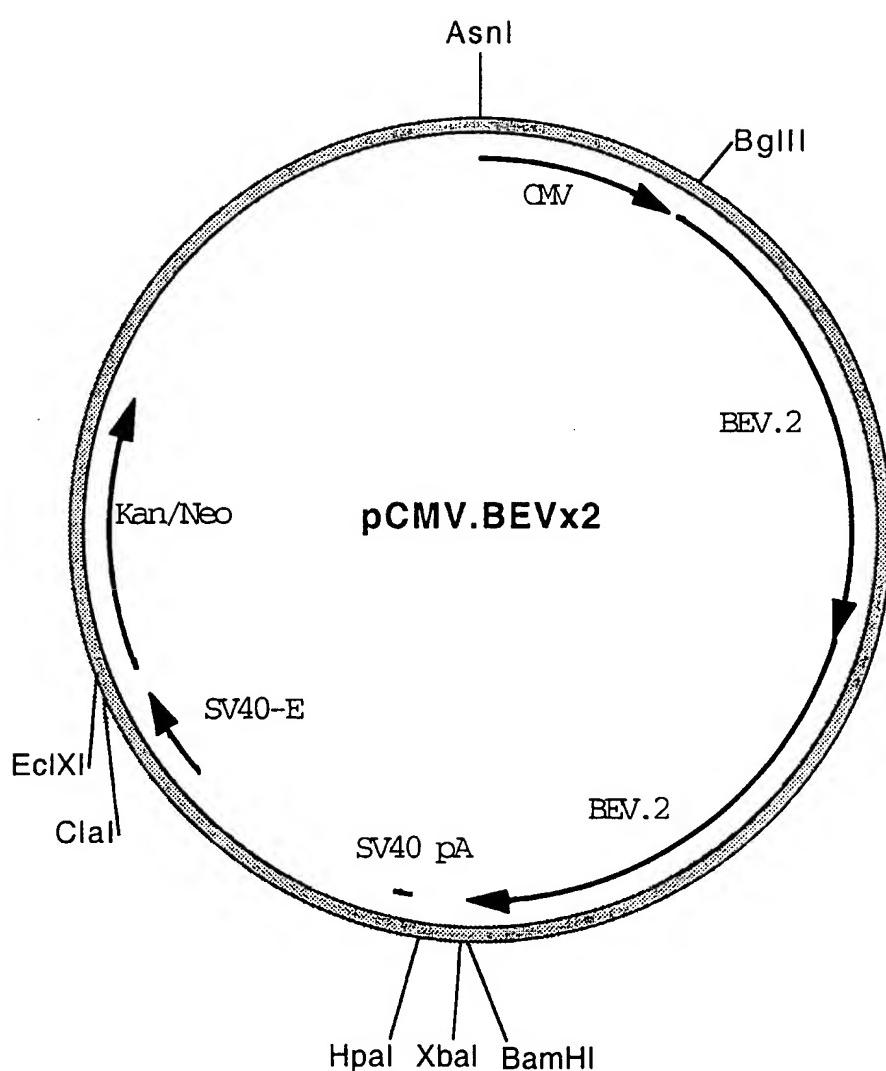


FIGURE 20

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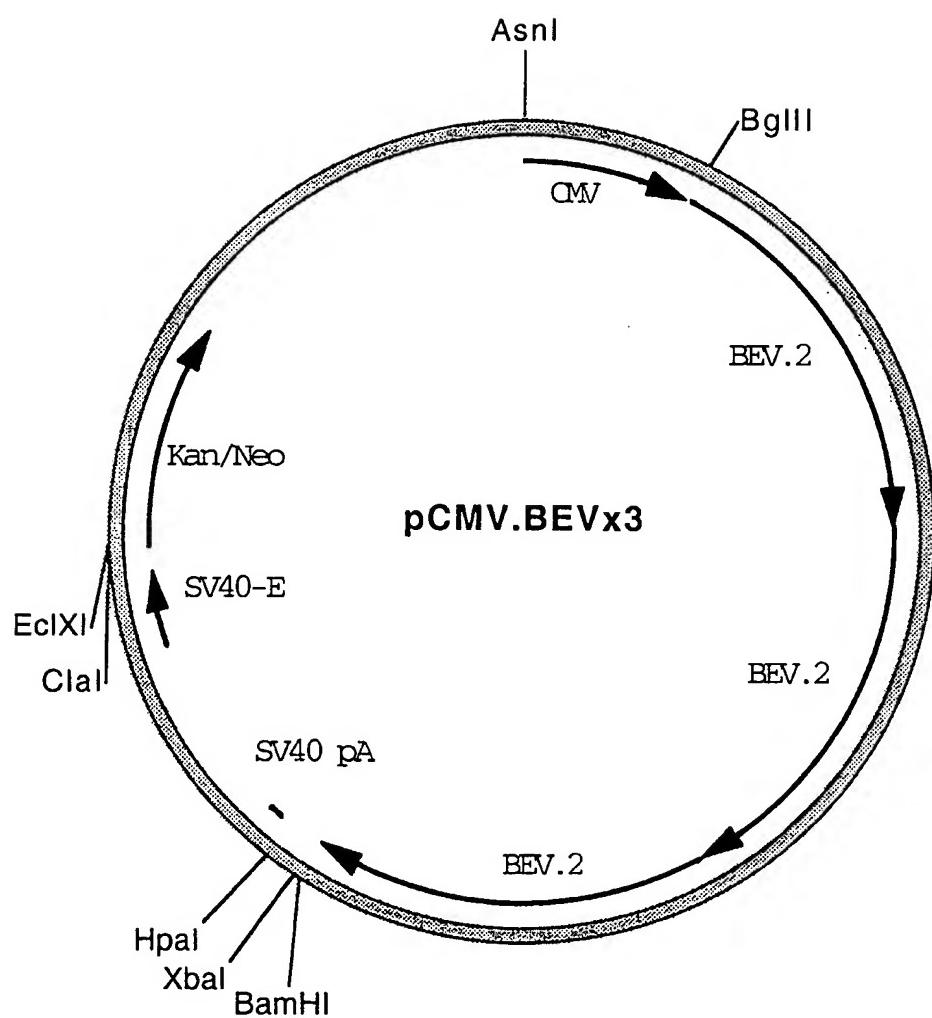
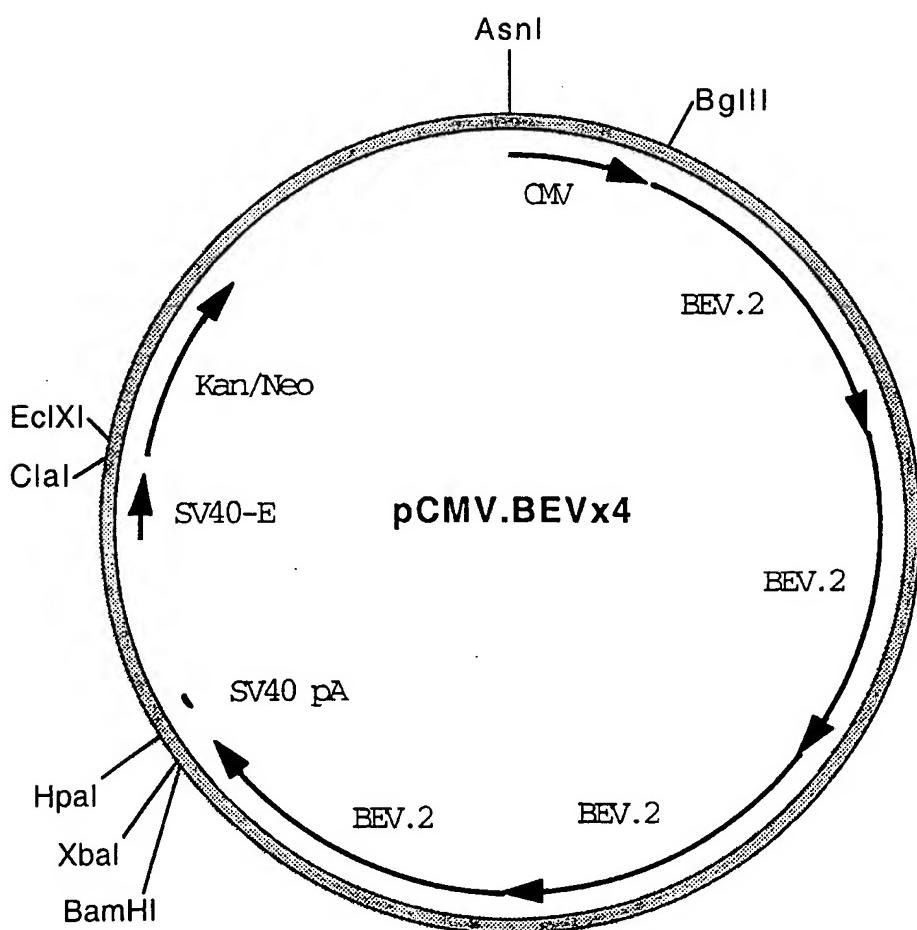
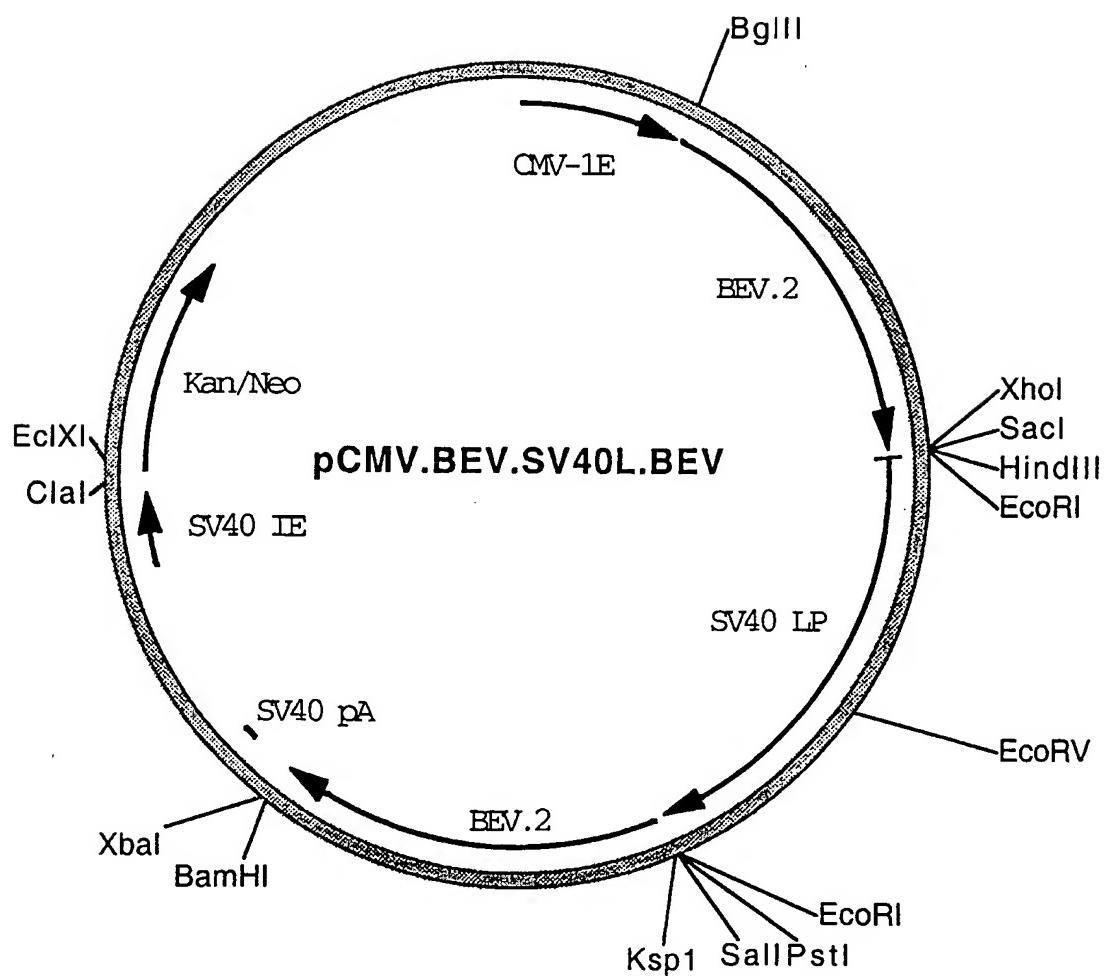


FIGURE 21

**FIGURE 22**

**FIGURE 23**

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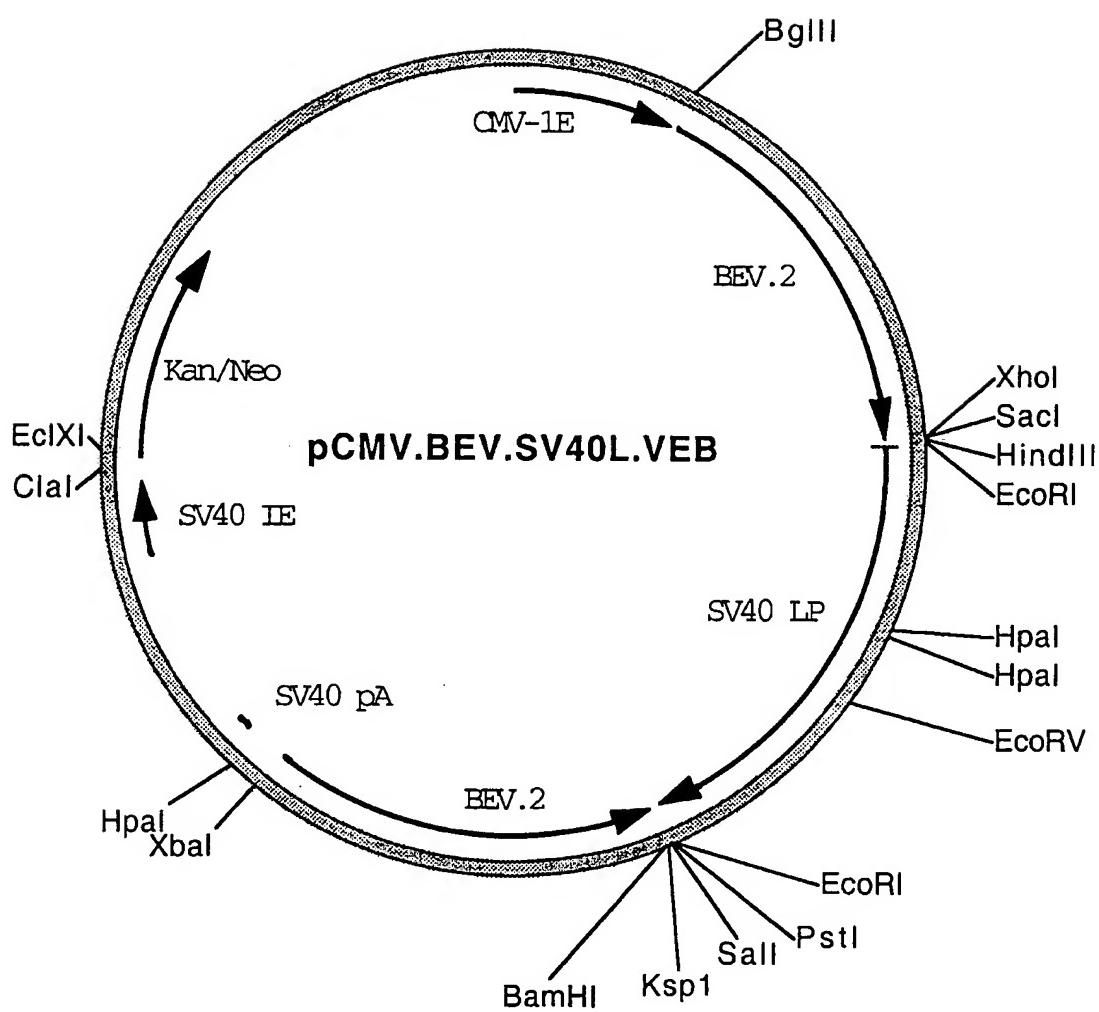
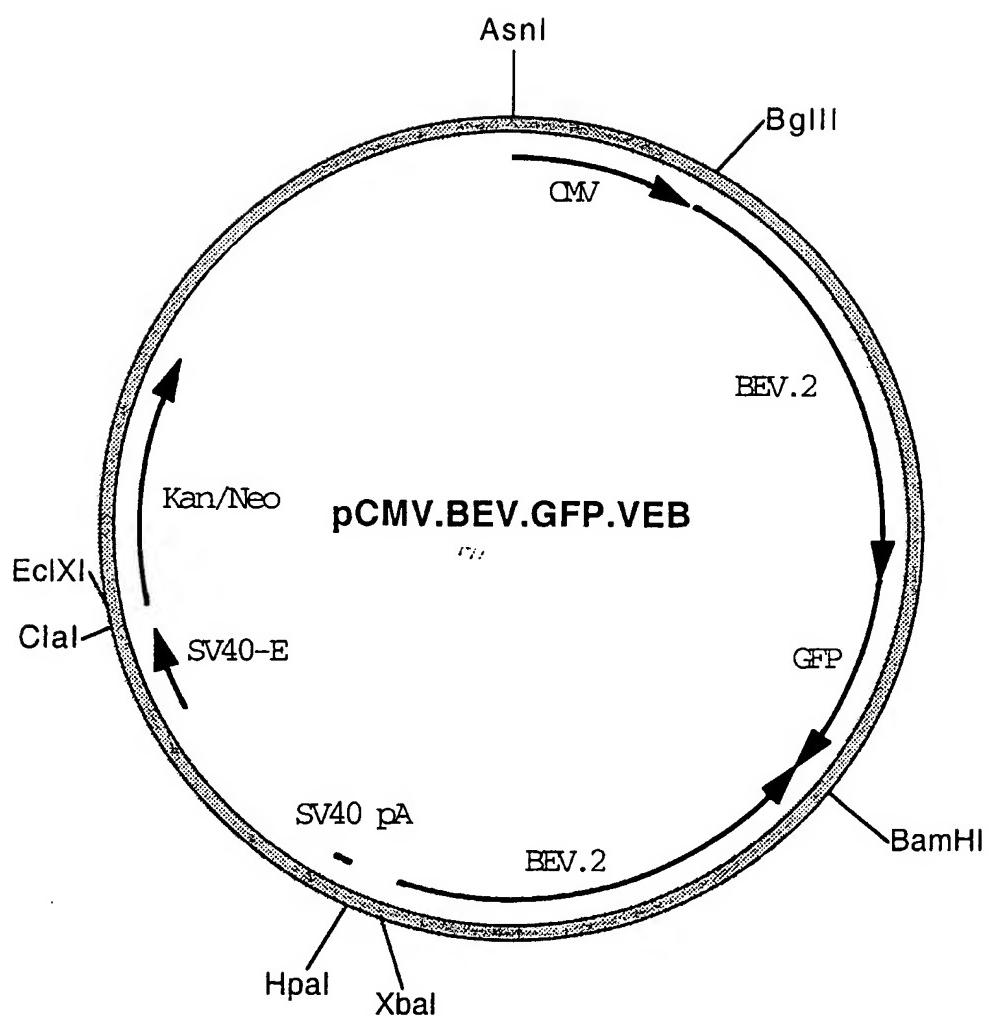
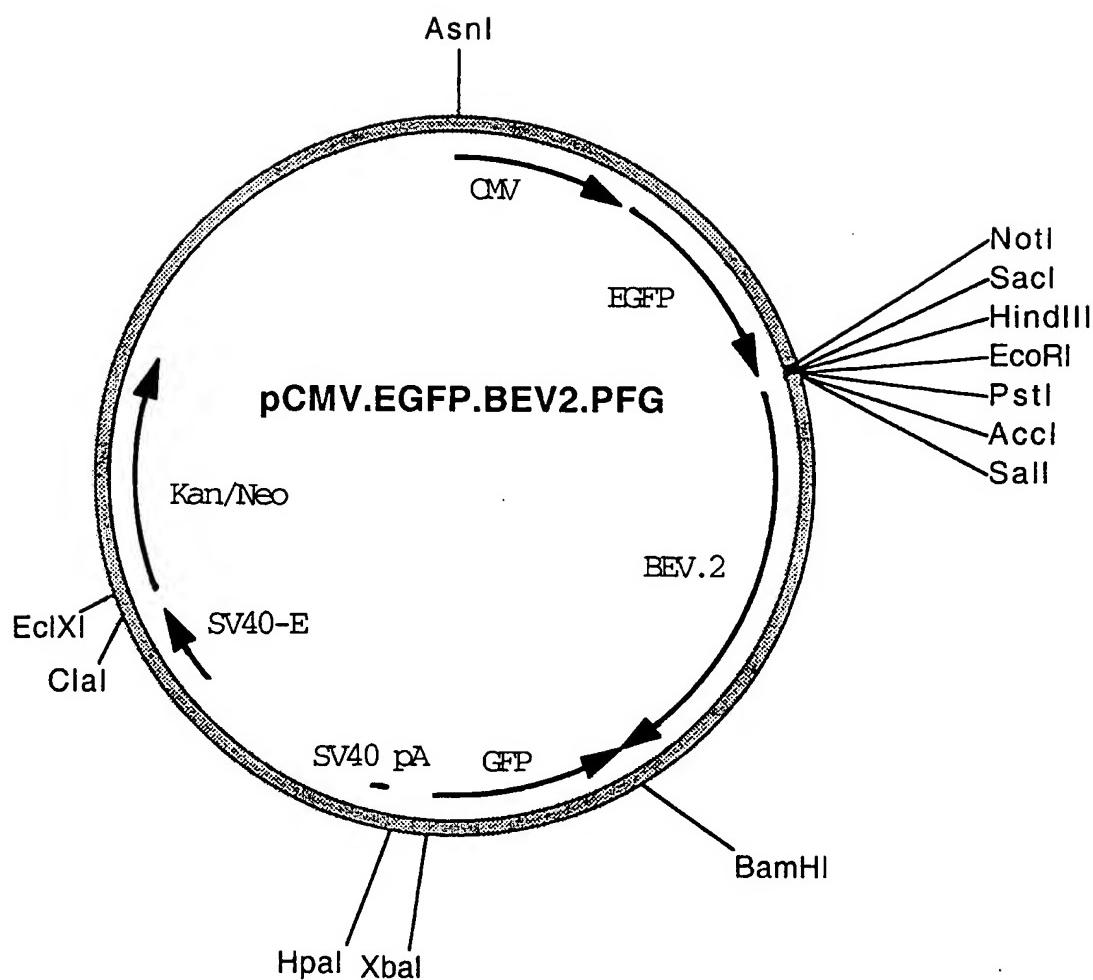
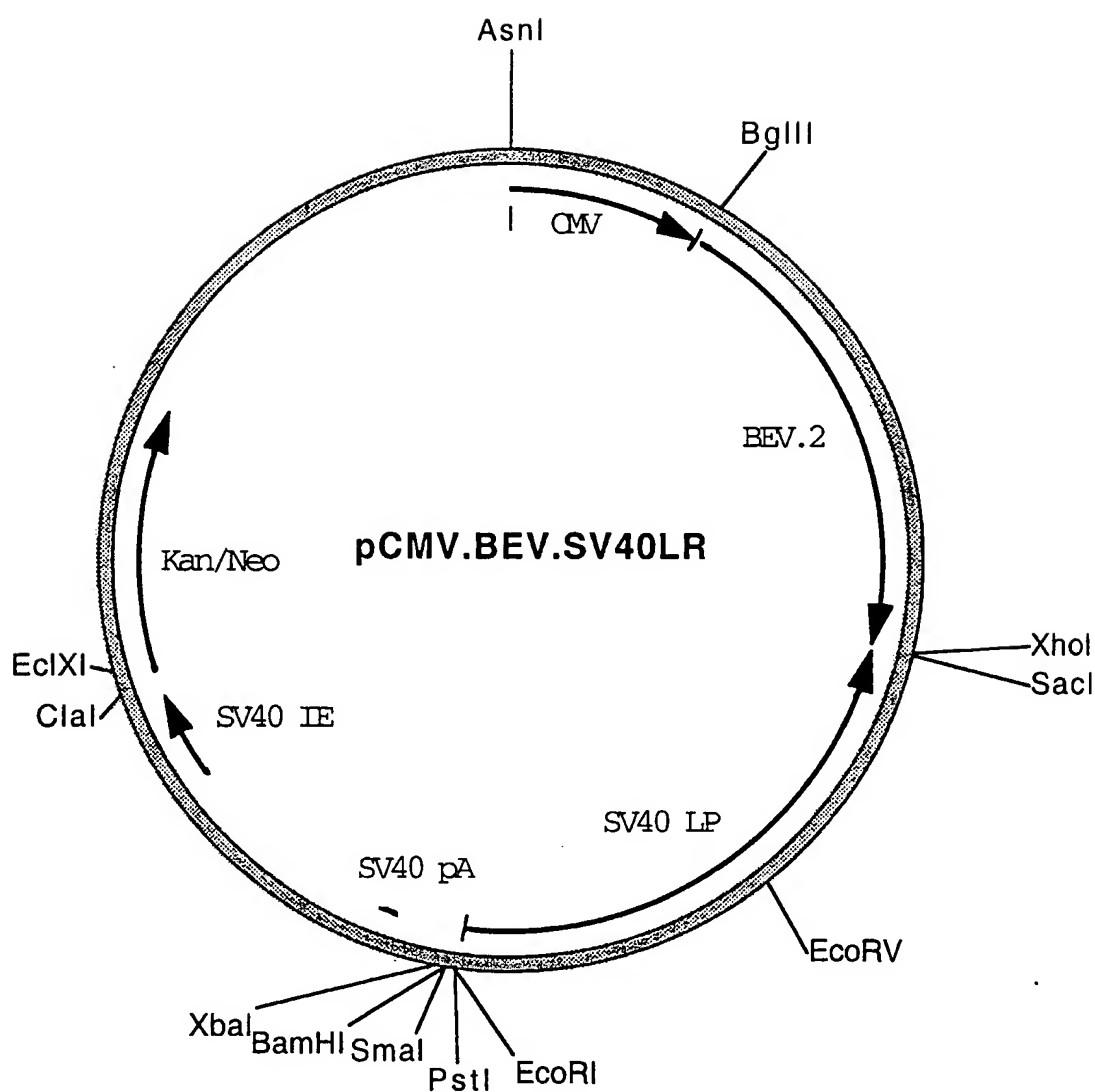


FIGURE 24

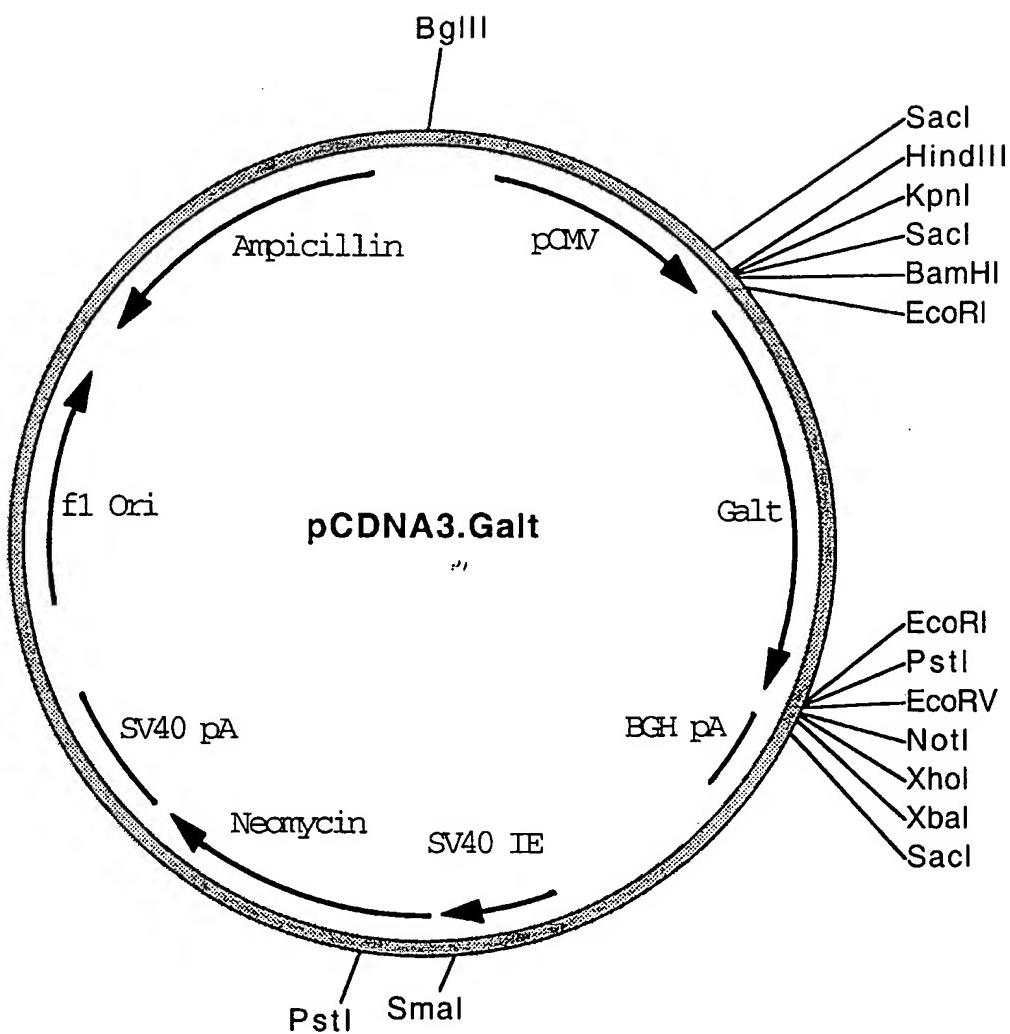
**FIGURE 25**

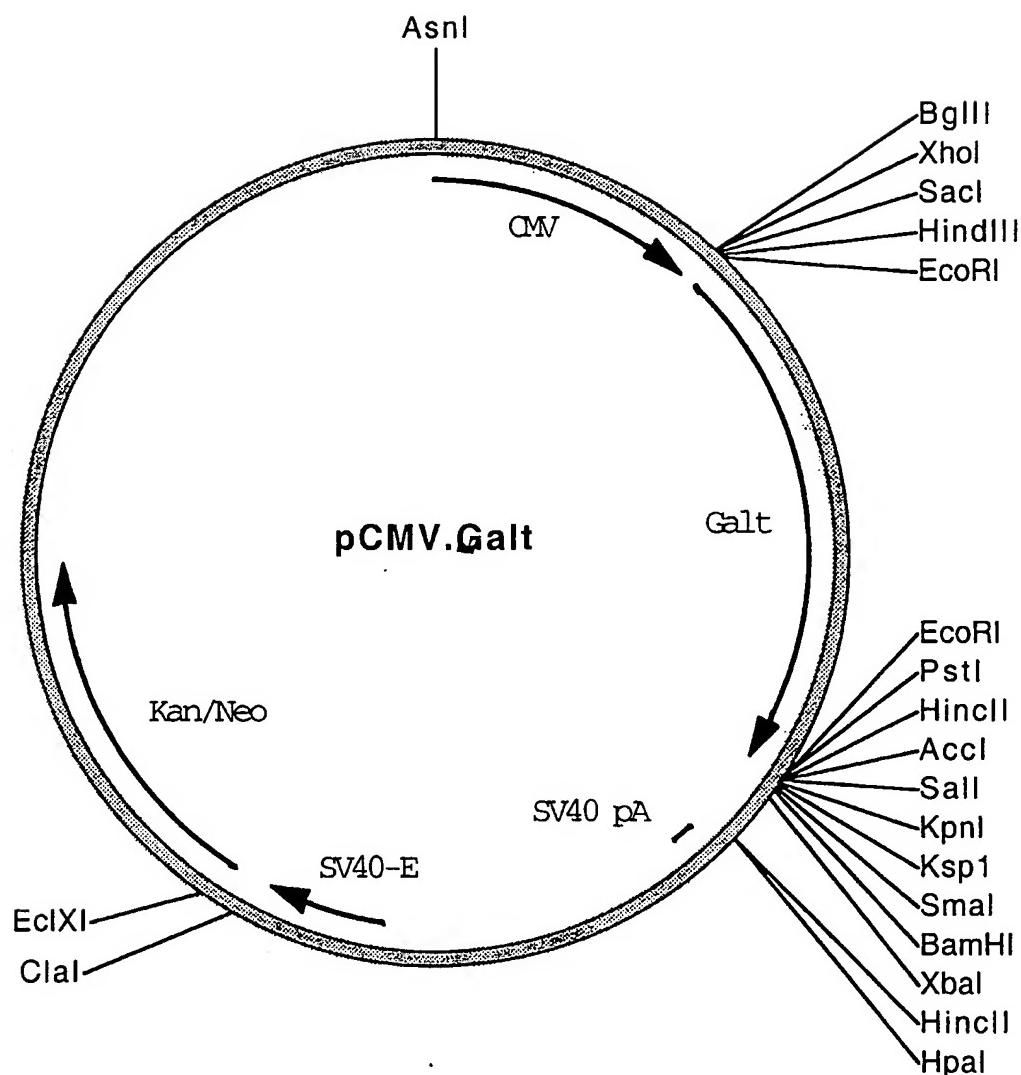
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**FIGURE 26**

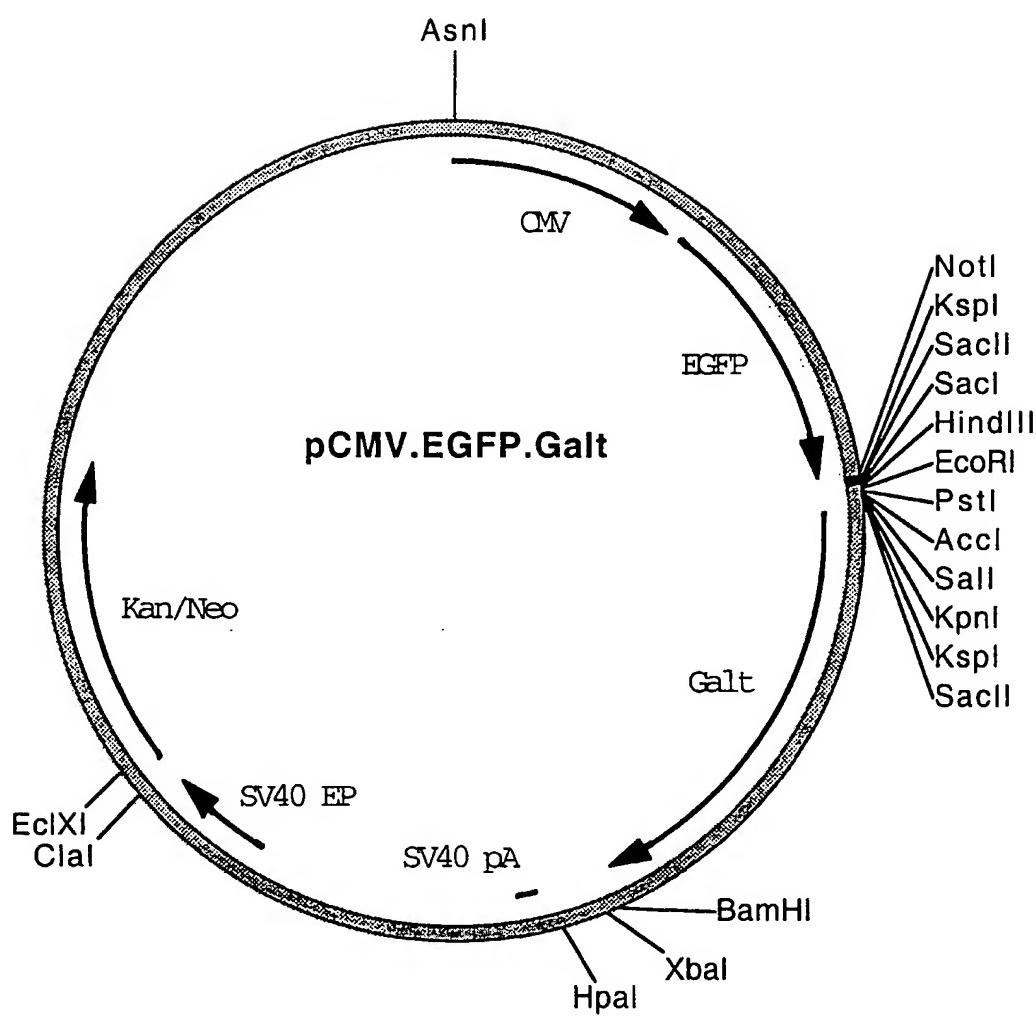
**FIGURE 27**

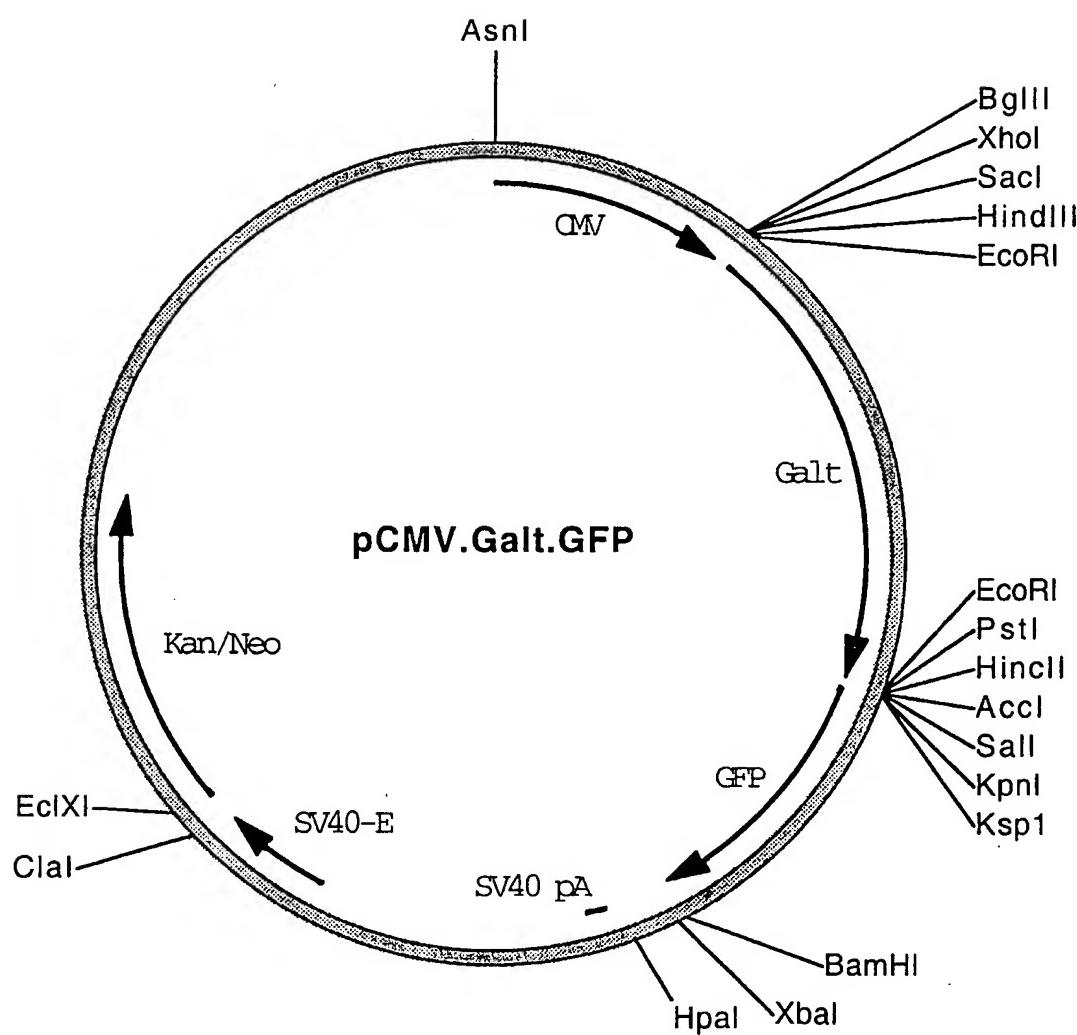
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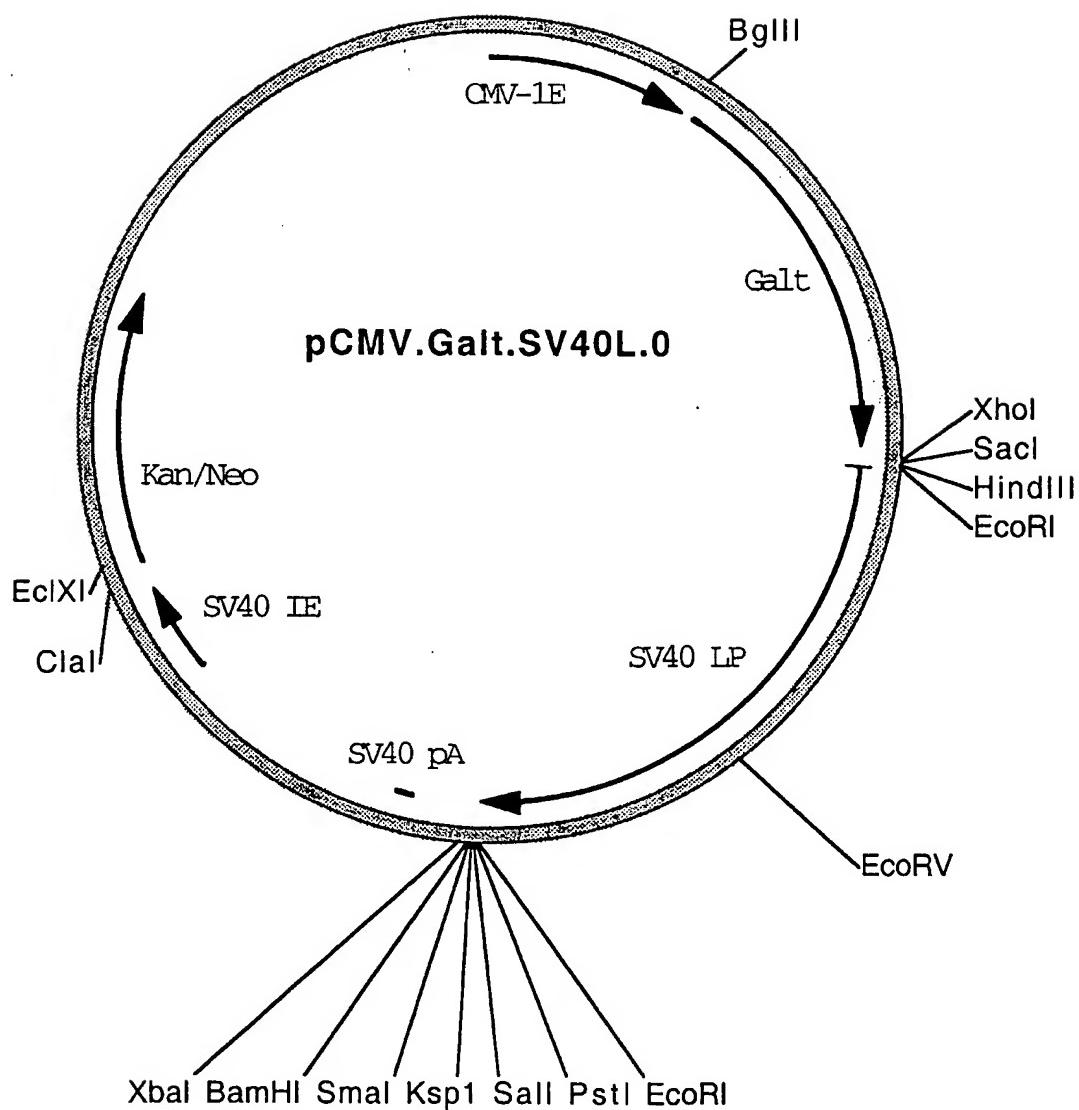
**FIGURE 28**

**FIGURE 29**

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**FIGURE 30**

**FIGURE 31**

**FIGURE 32**

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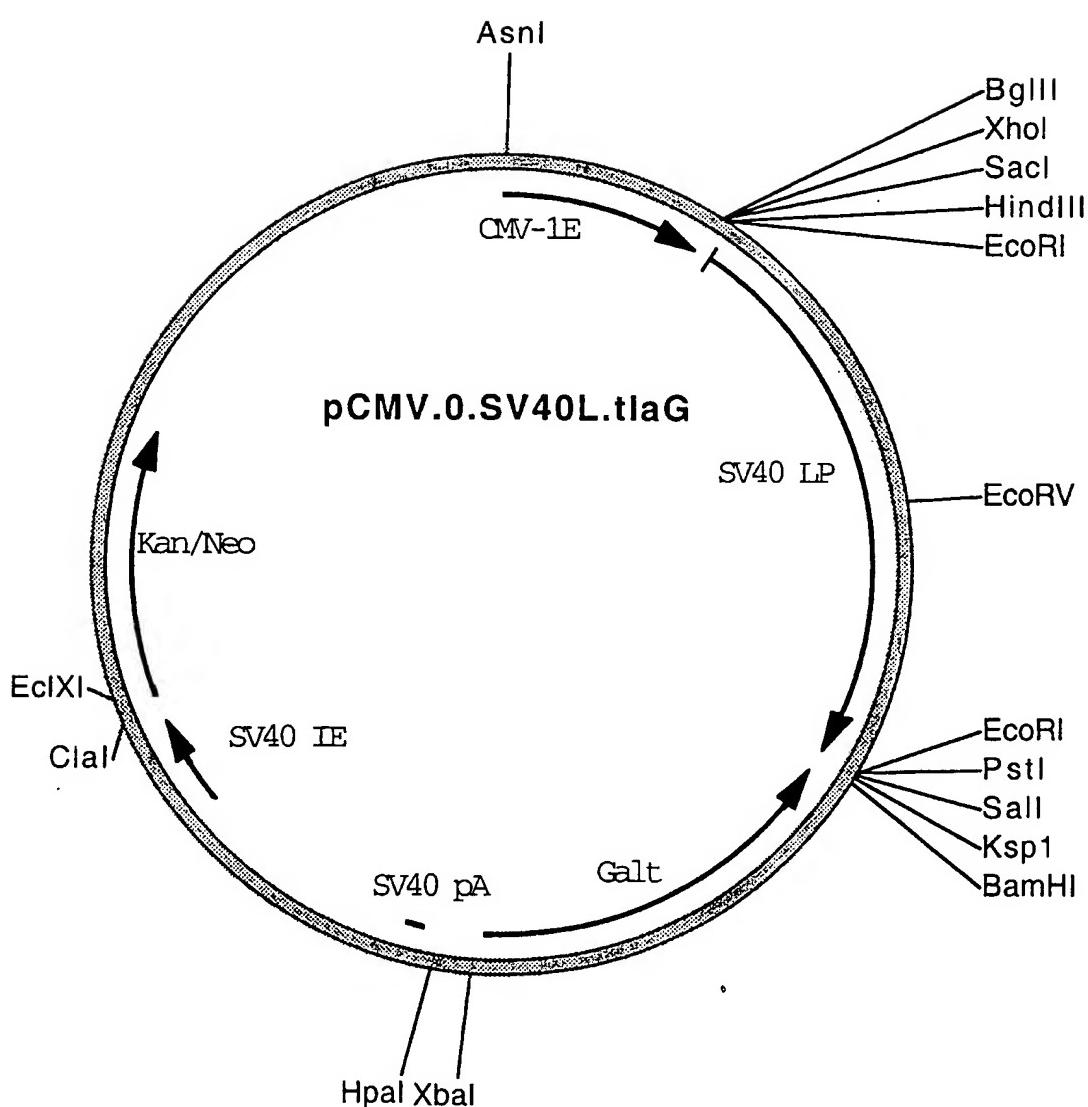
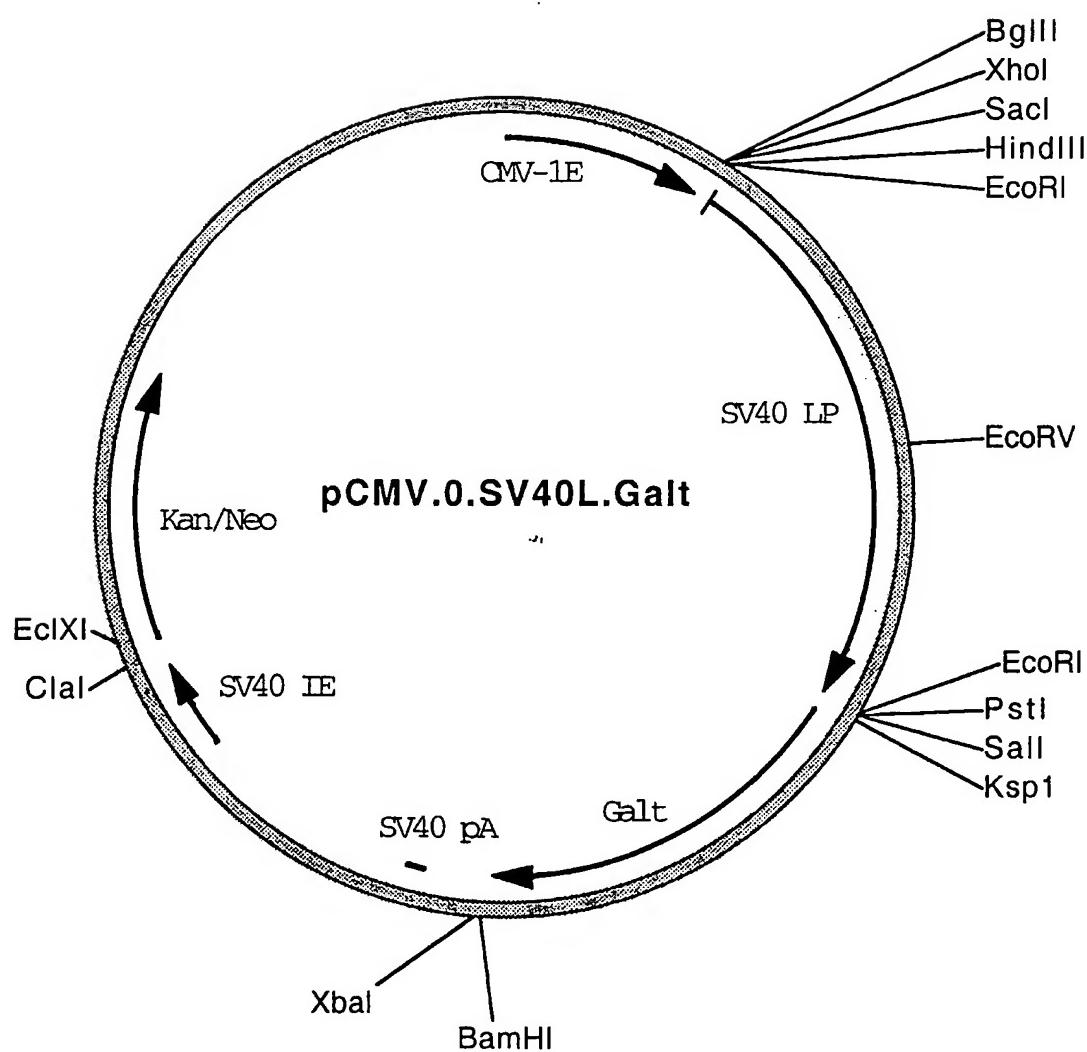


FIGURE 33

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**FIGURE 34**

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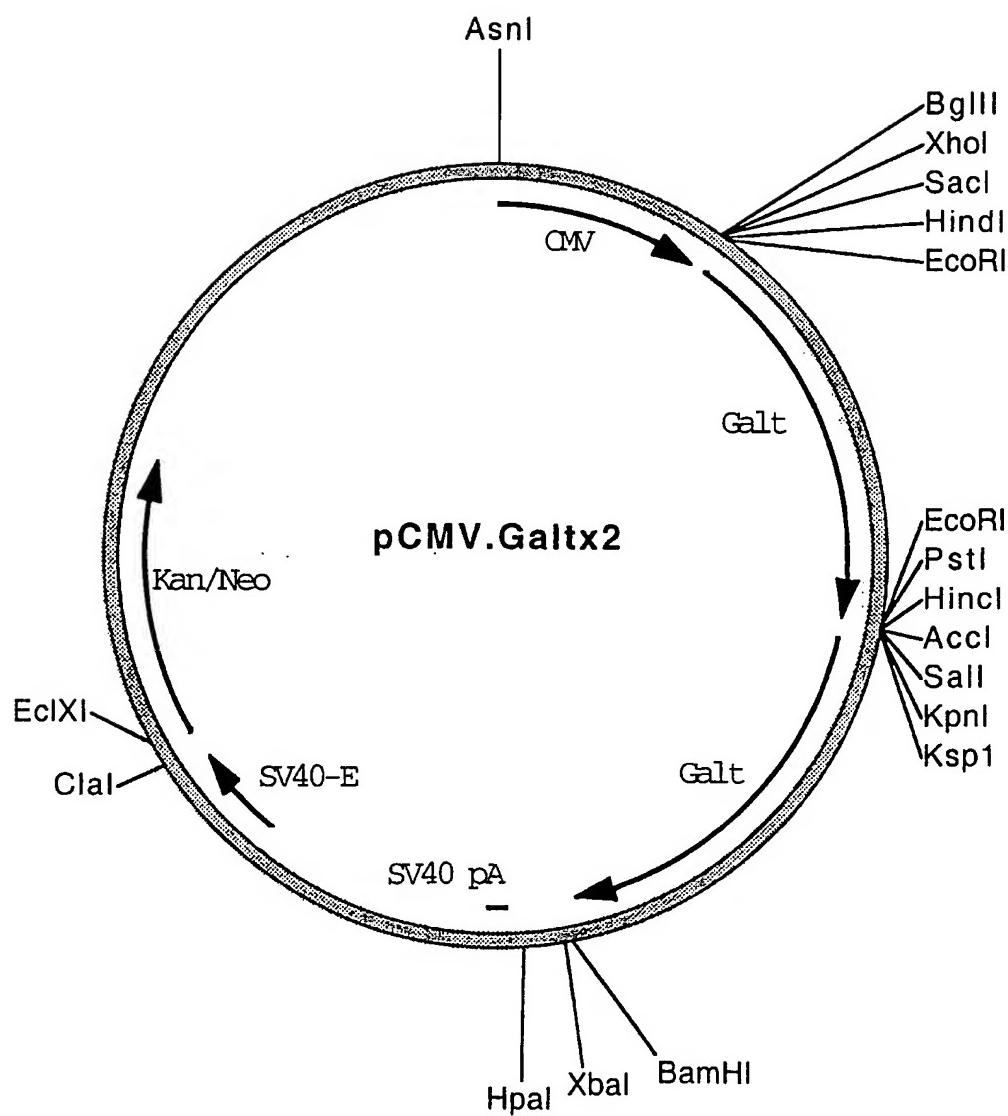
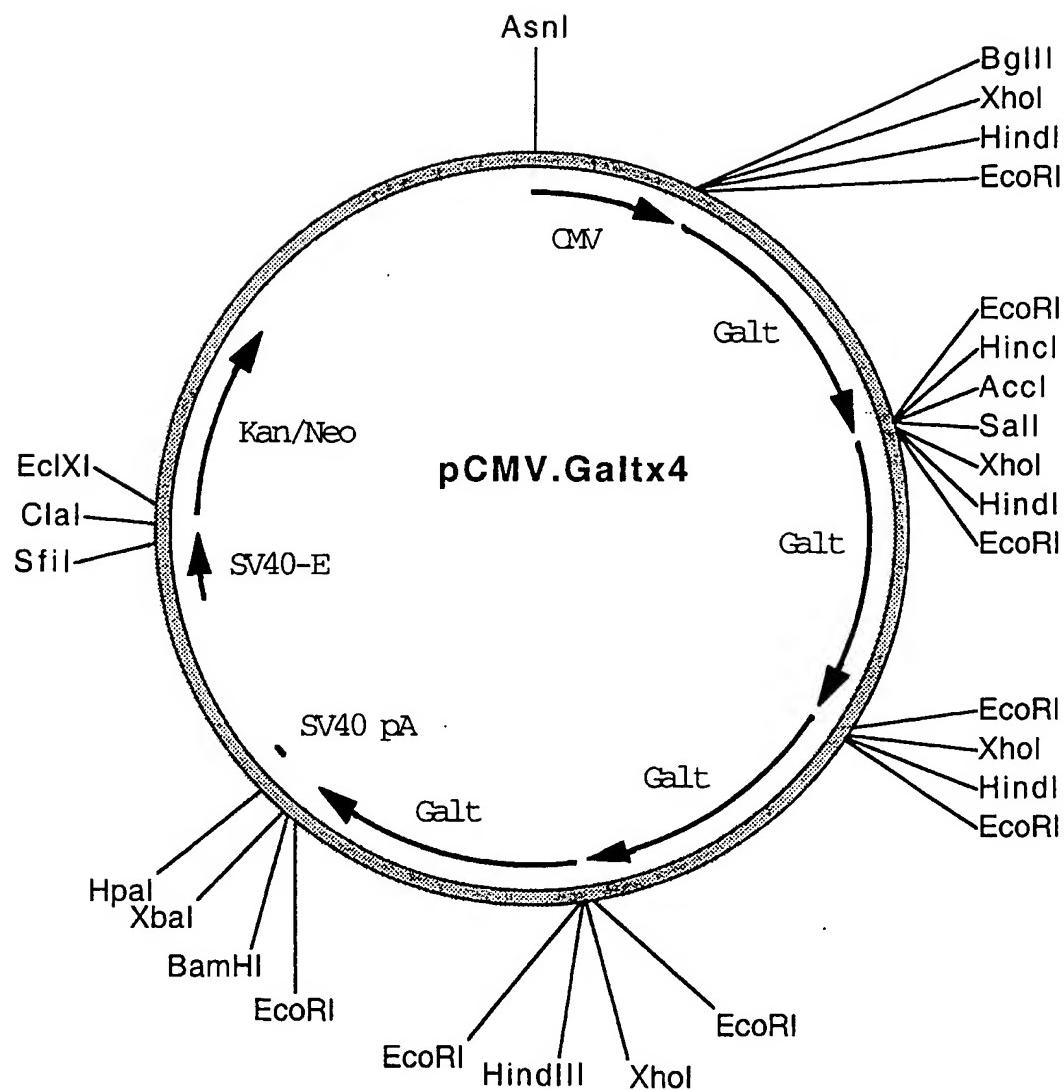
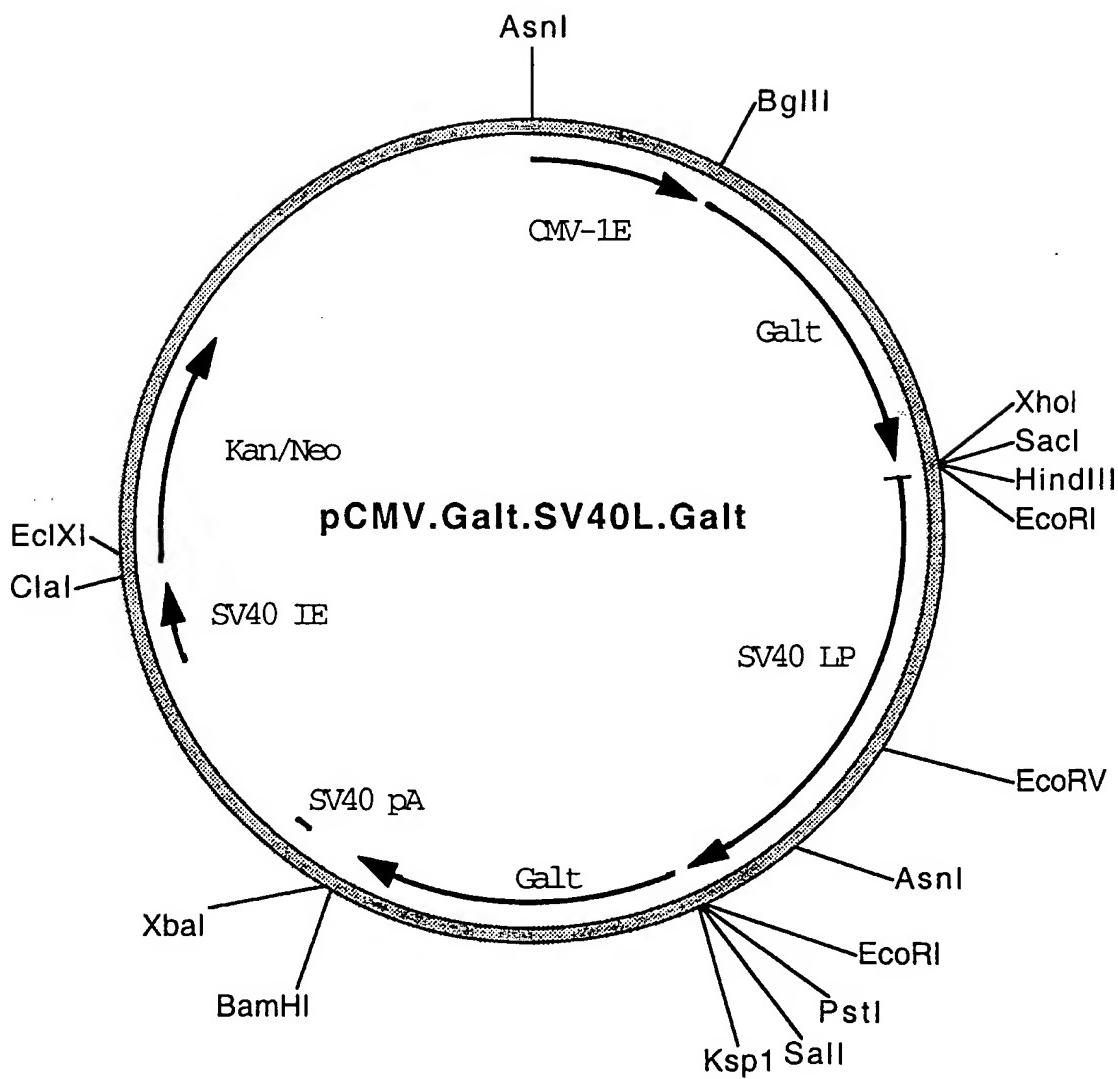


FIGURE 35

**FIGURE 36**

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**FIGURE 37**

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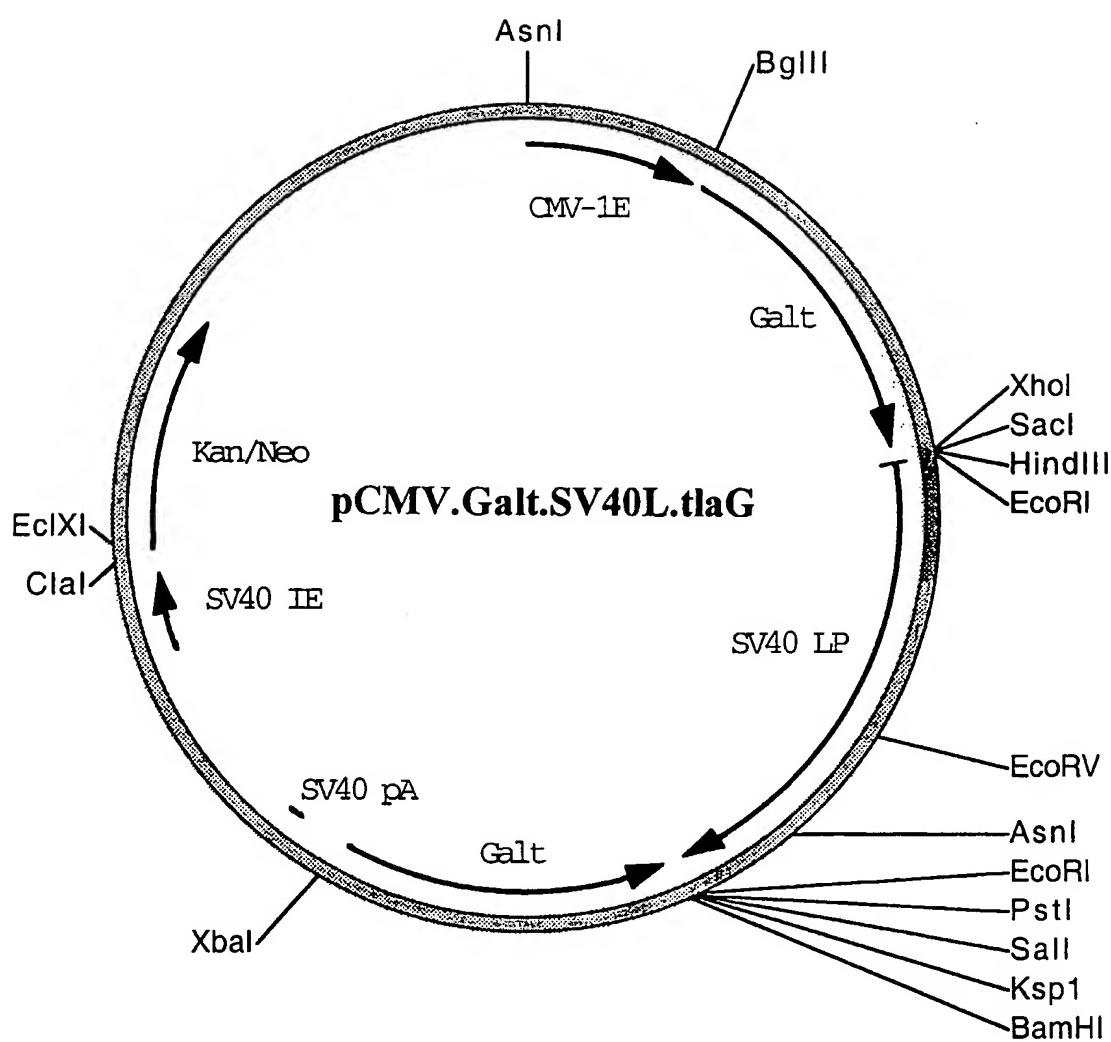
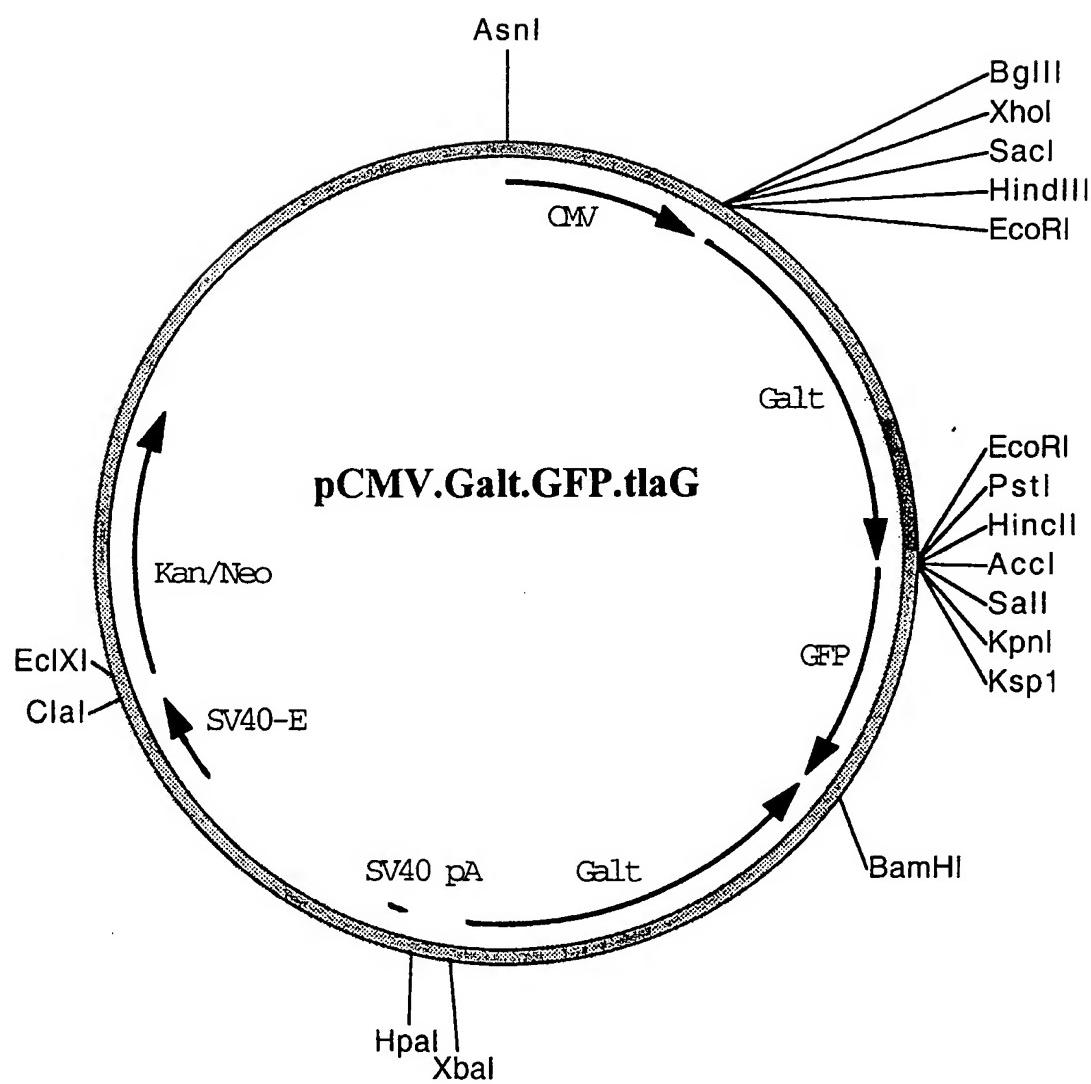
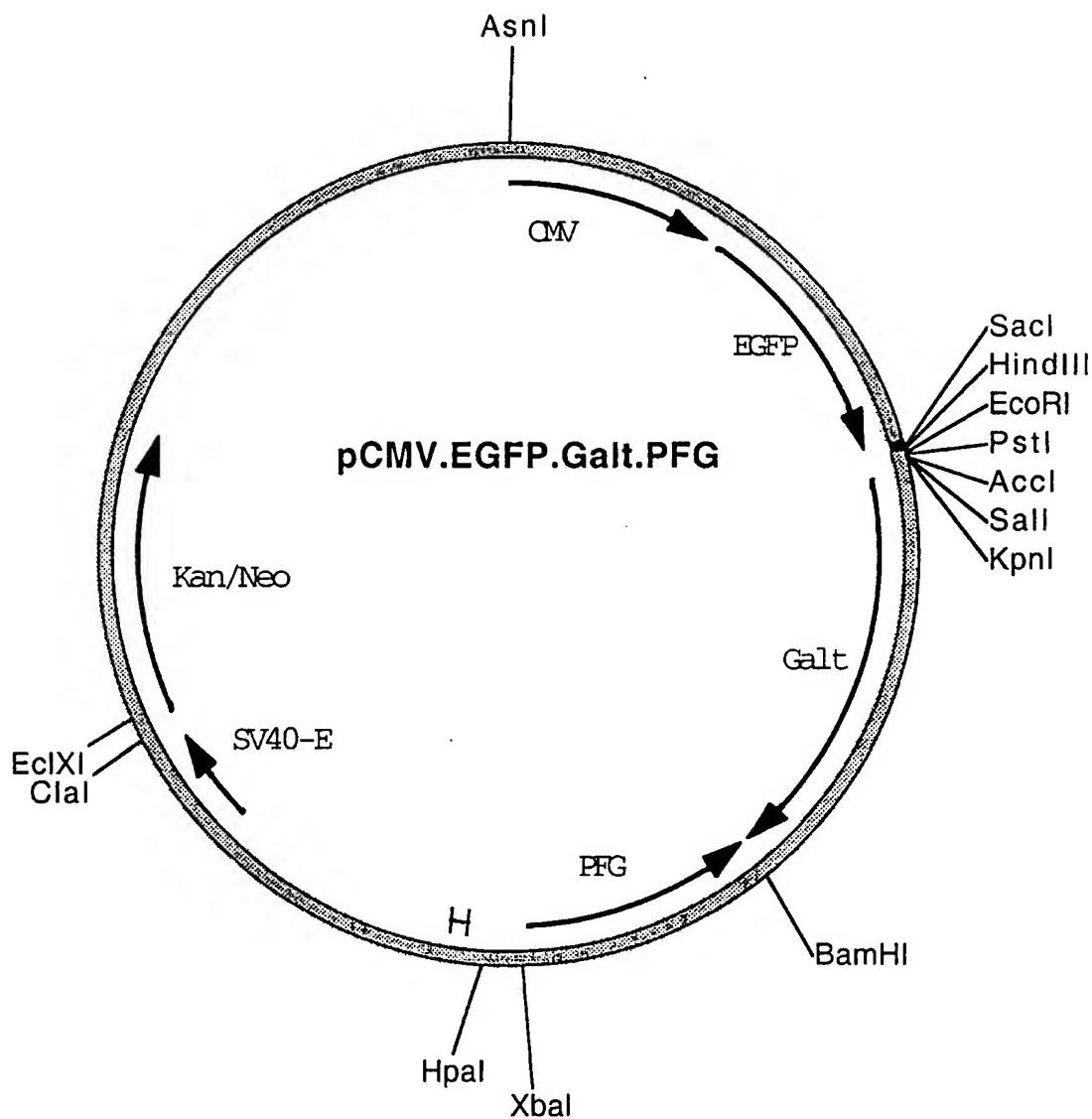
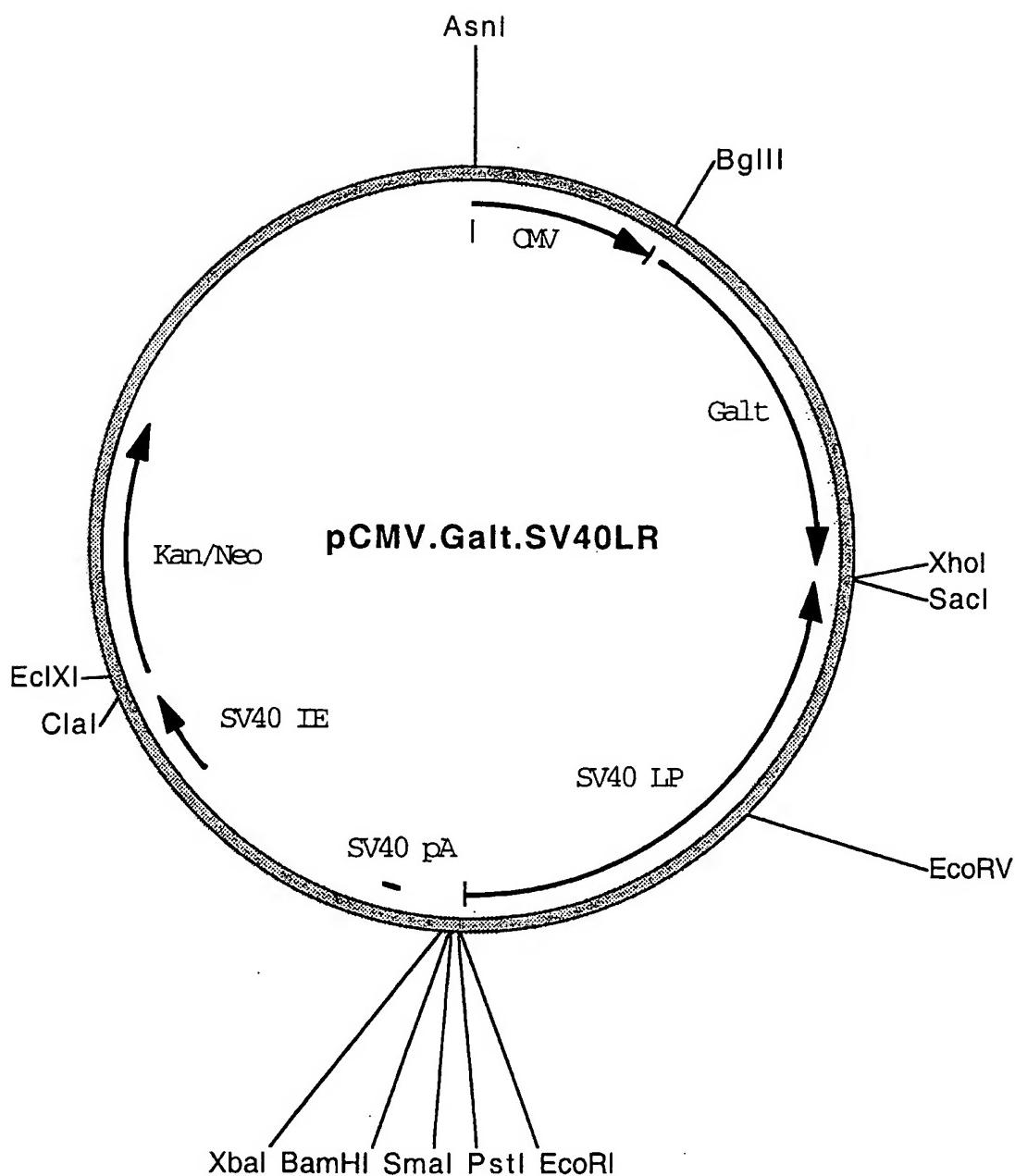


FIGURE 38

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**FIGURE 39**

**FIGURE 40**

**FIGURE 41**

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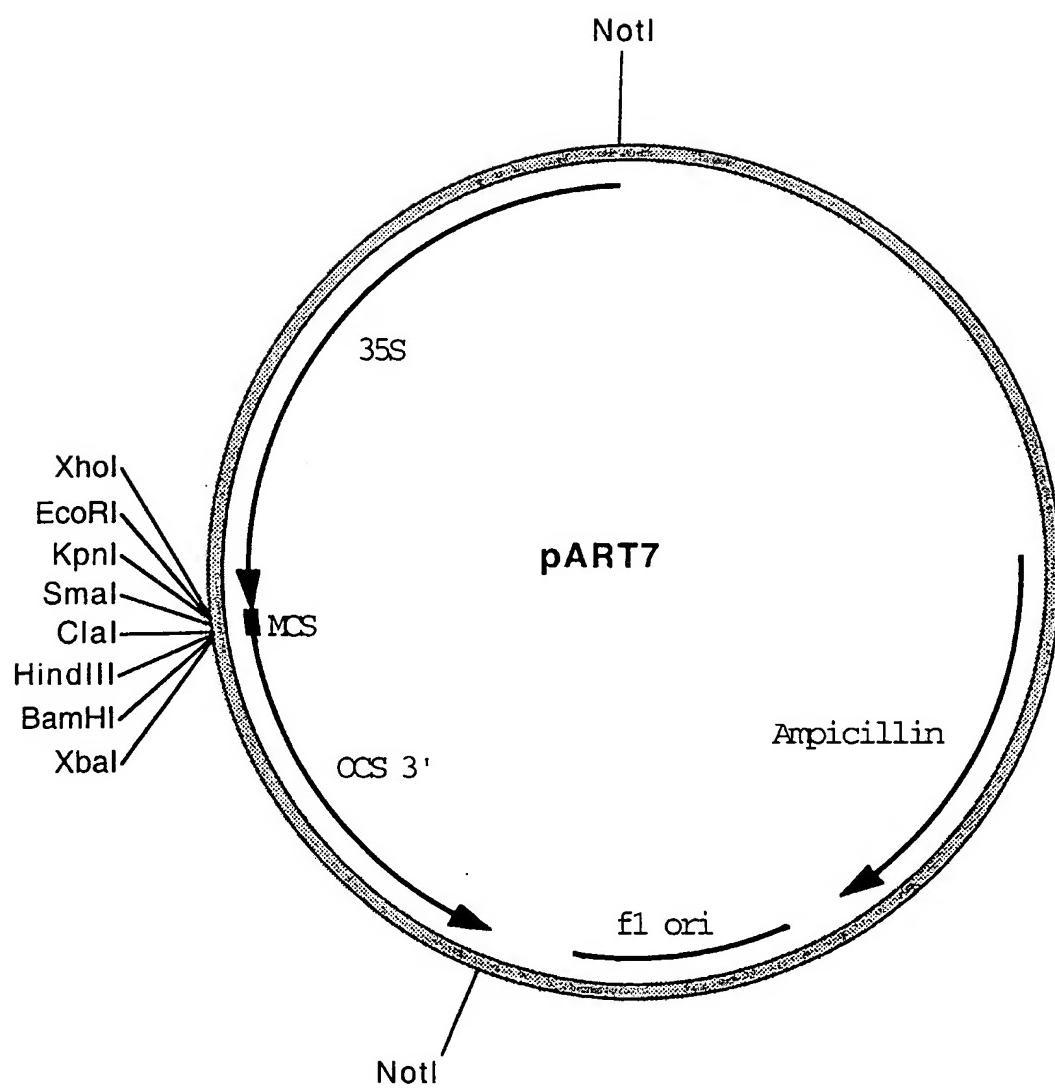
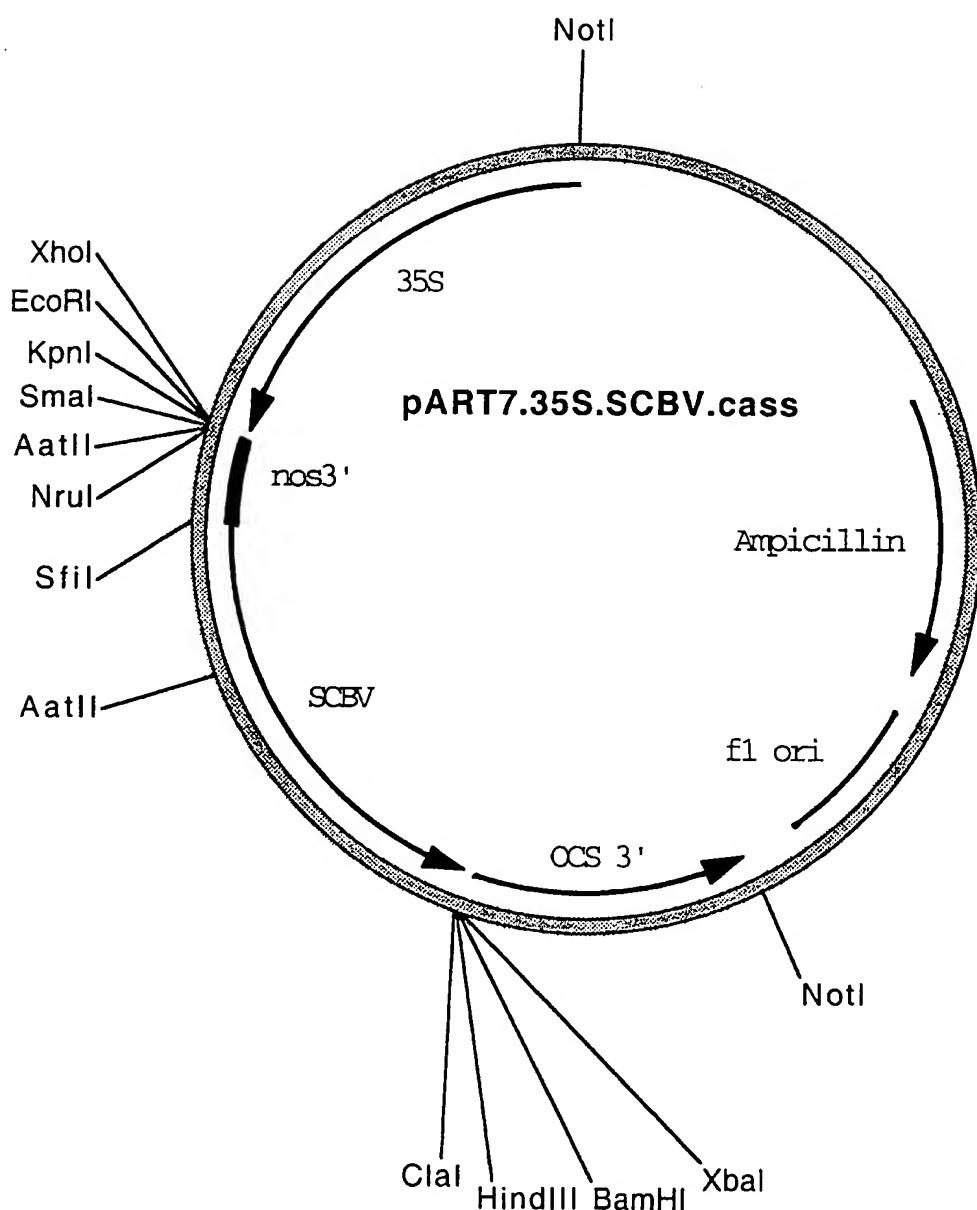
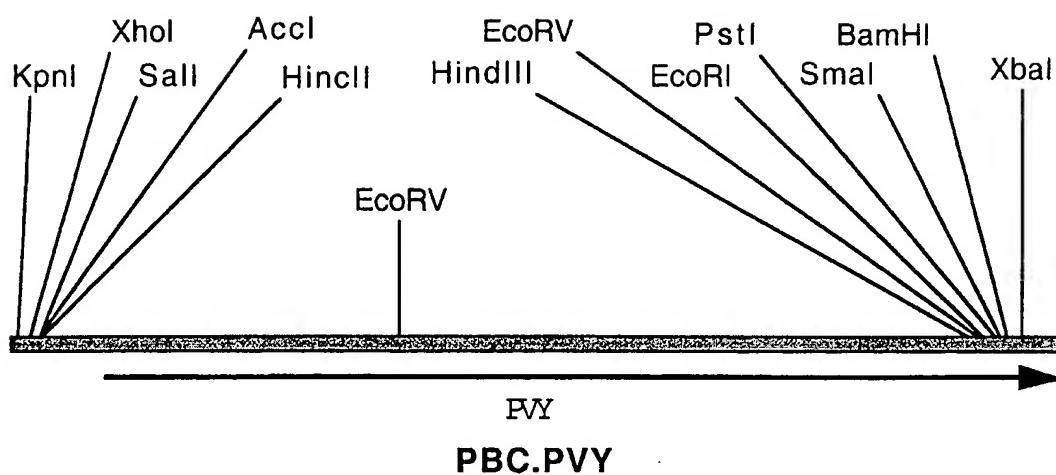


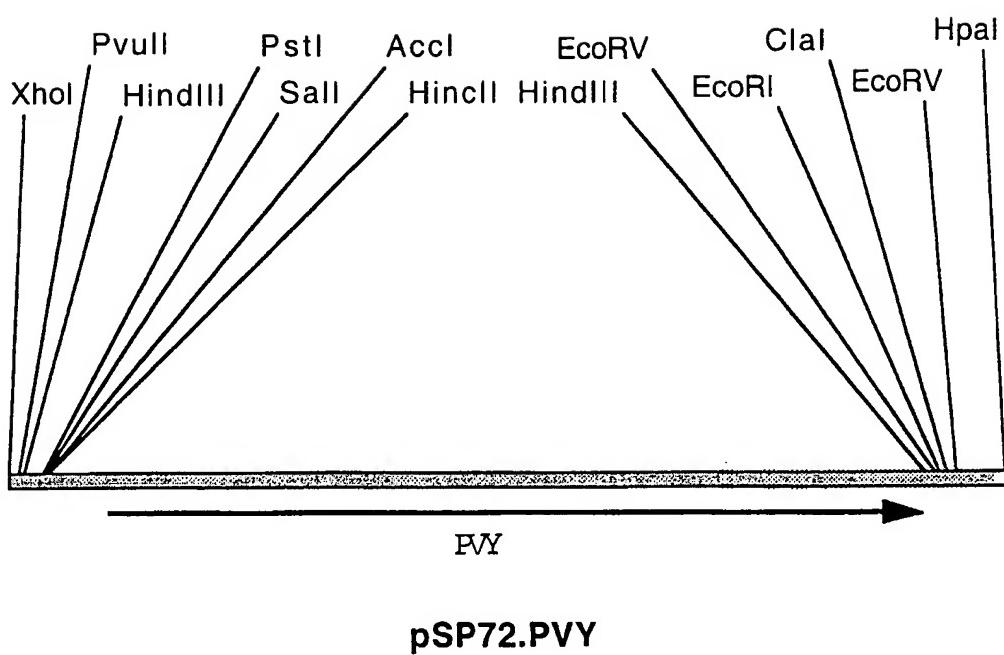
FIGURE 42

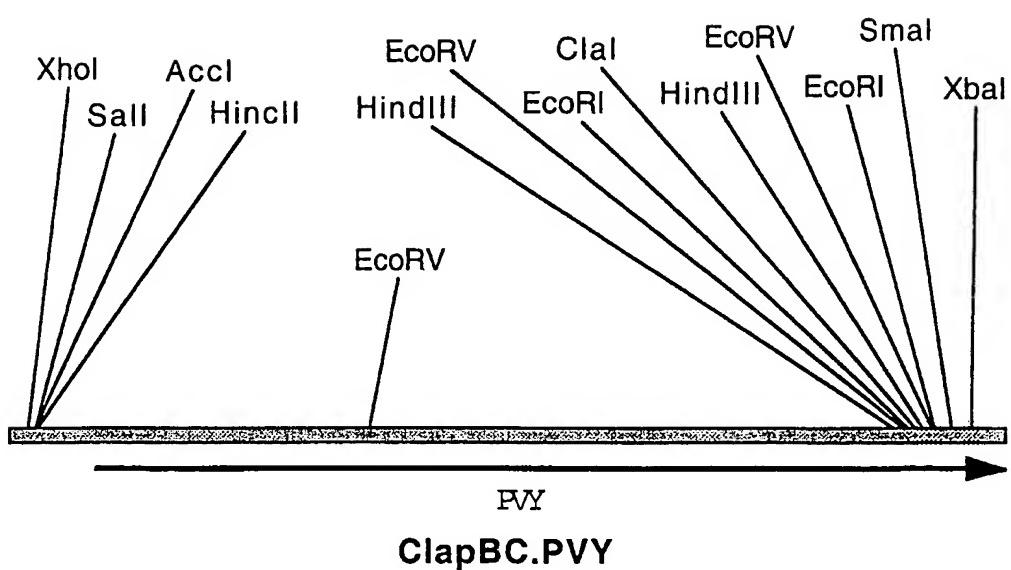
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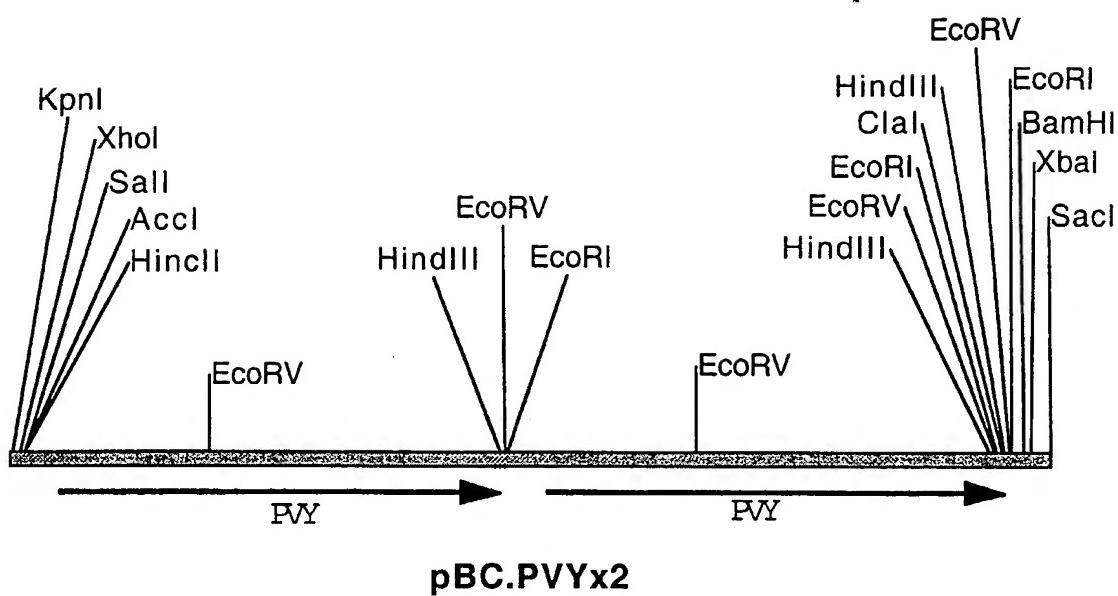
**FIGURE 43**

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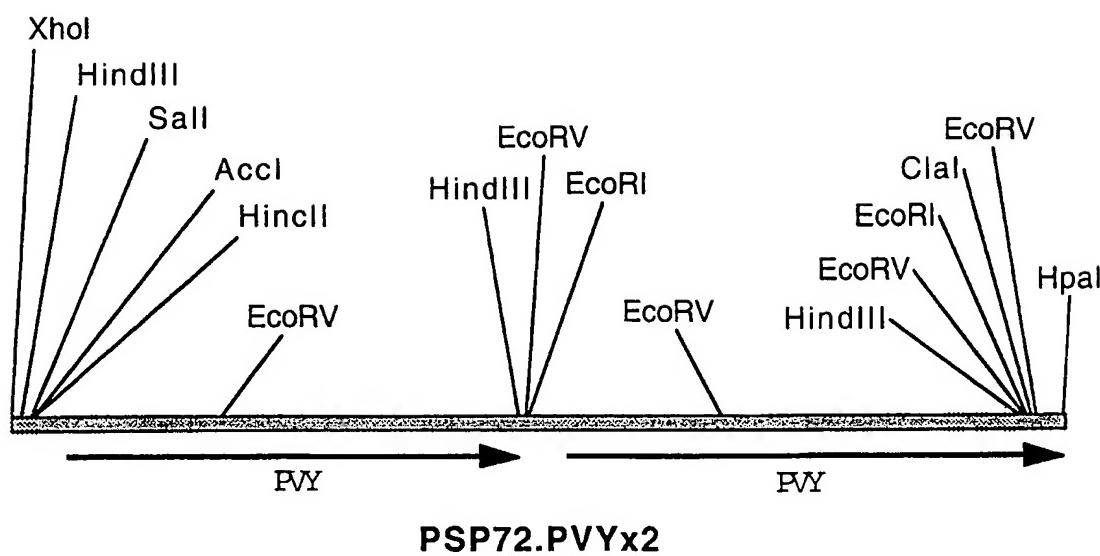
**FIGURE 44**

**45/68****FIGURE 45**

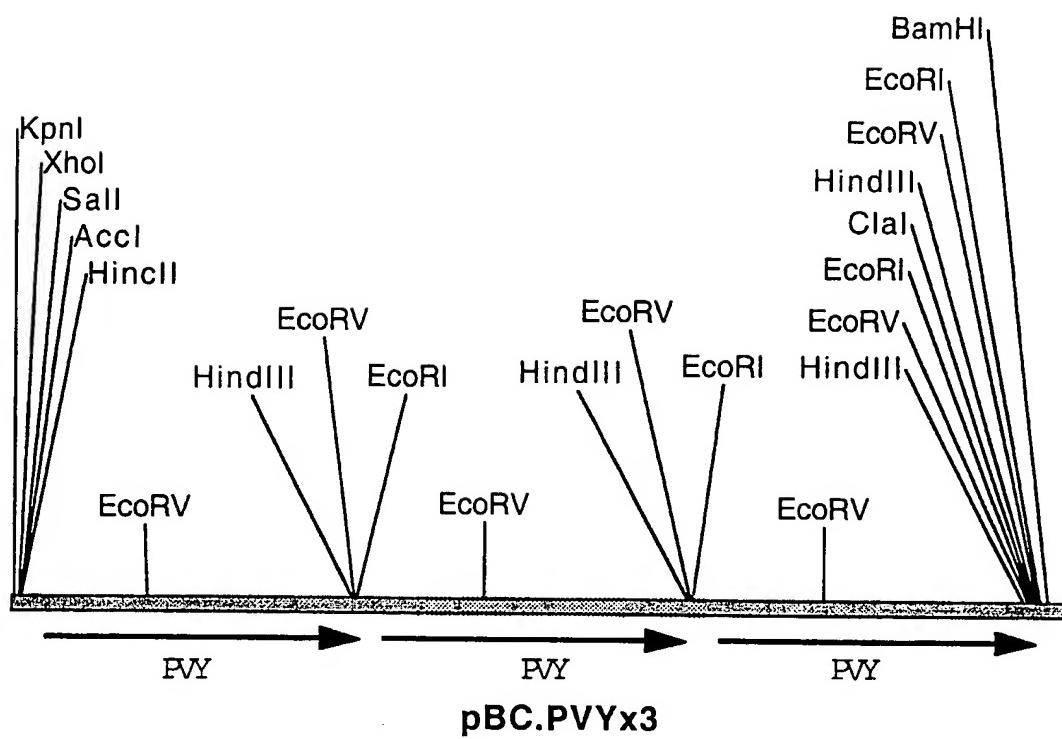
**46/68****FIGURE 46**

**47/68****FIGURE 47**

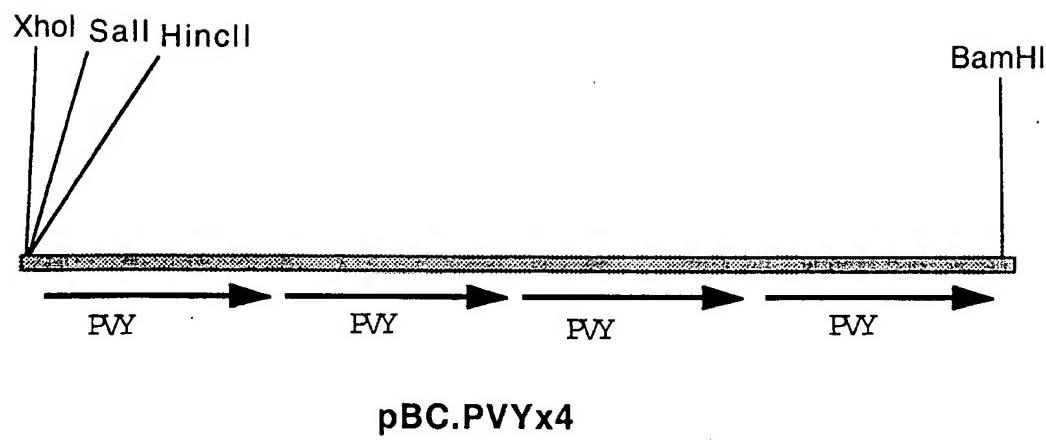
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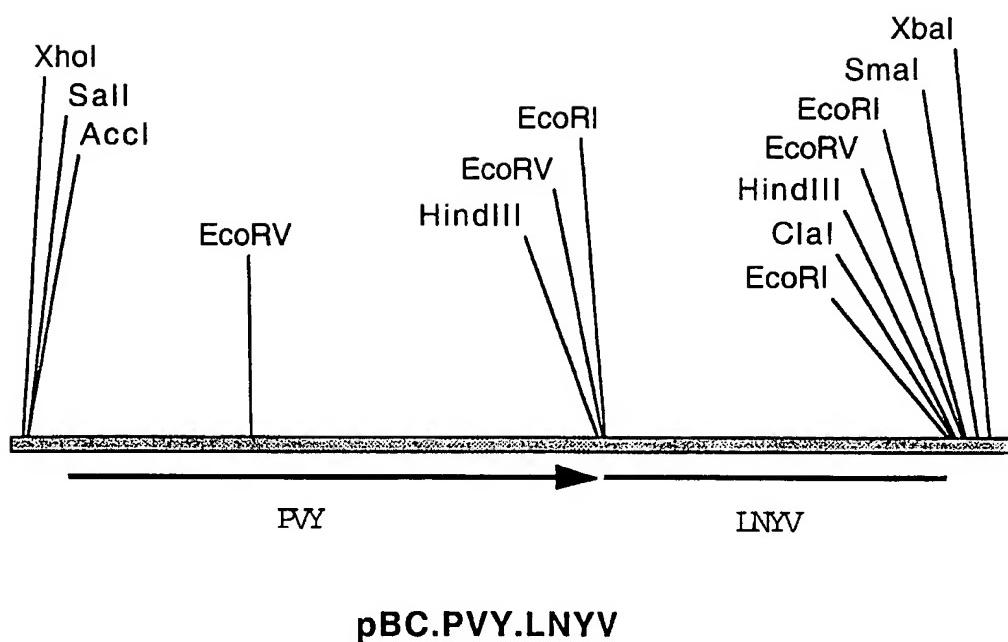
**FIGURE 48**

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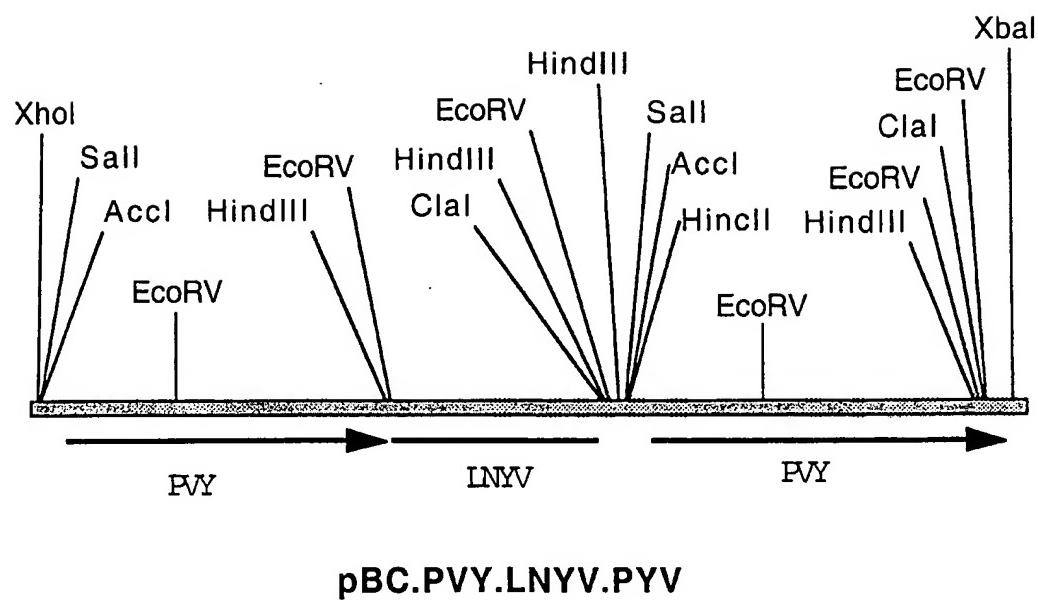
**FIGURE 49**

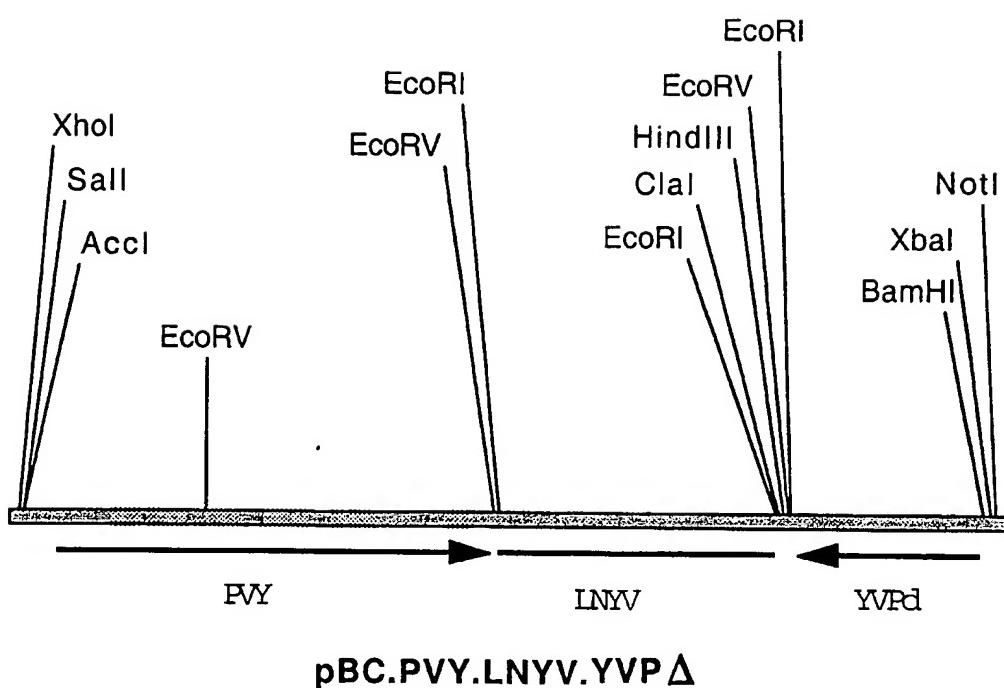
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**FIGURE 50**

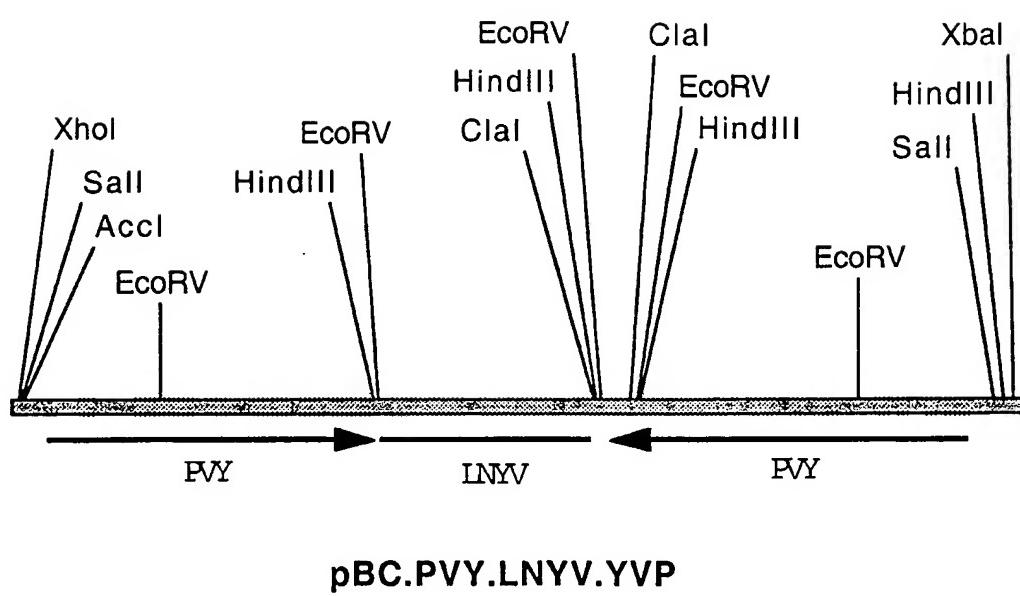
**FIGURE 51**

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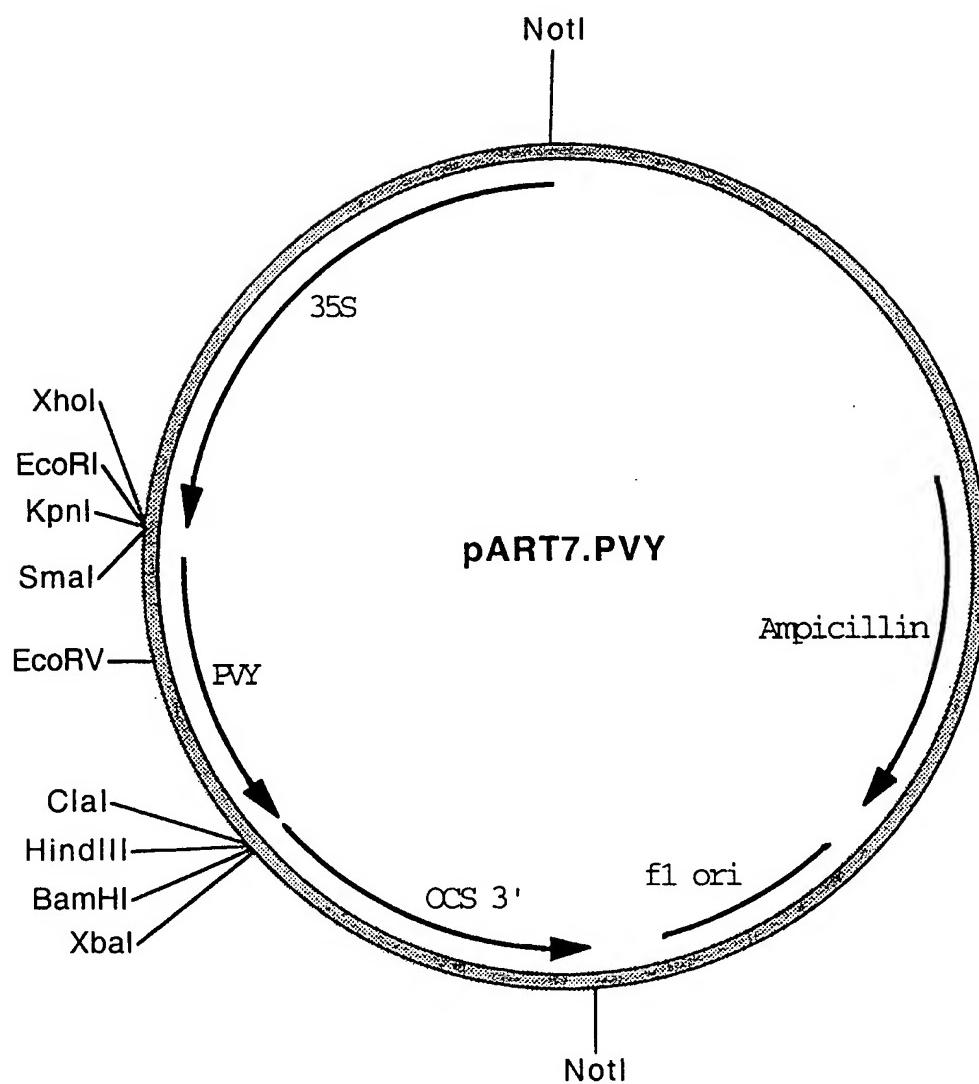
**FIGURE 52**

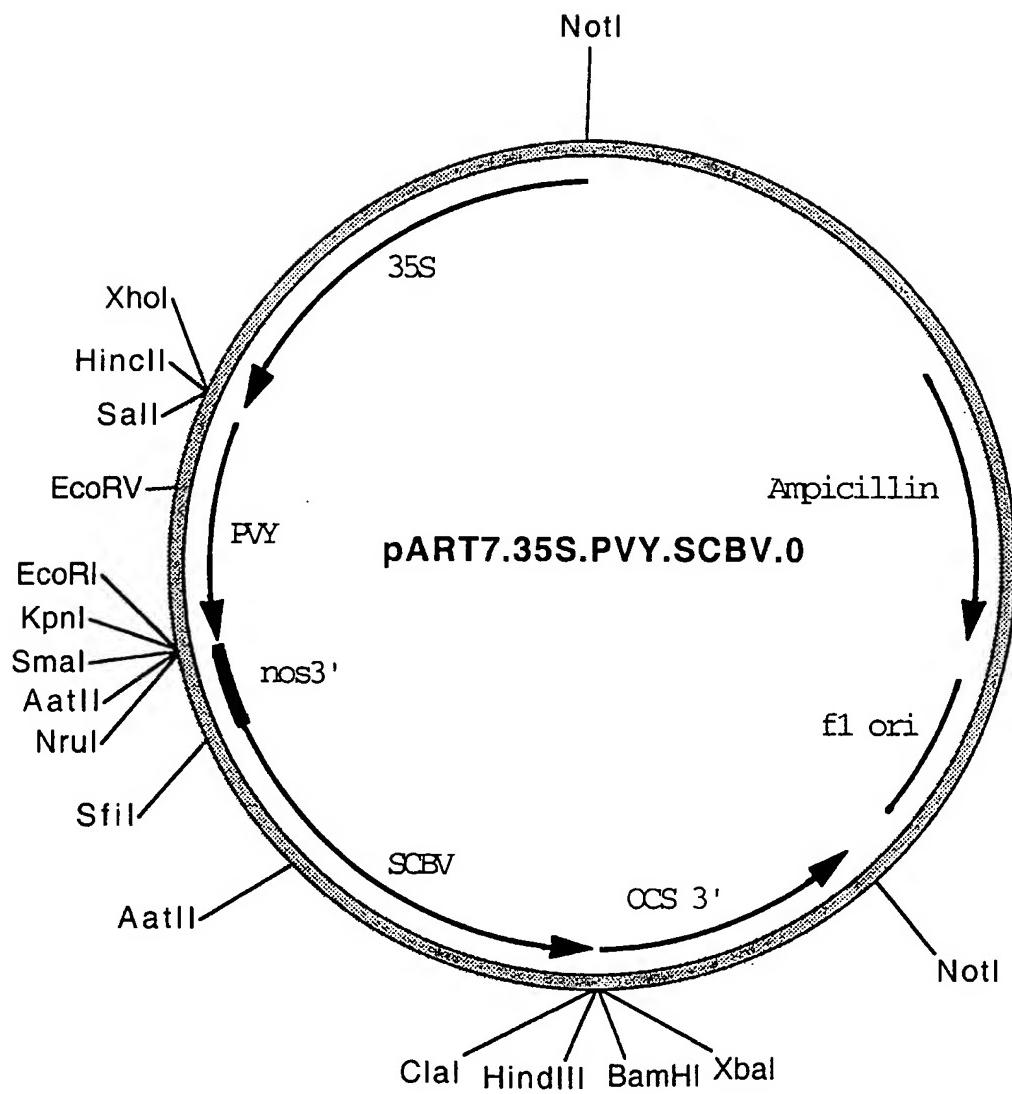
**FIGURE 53**

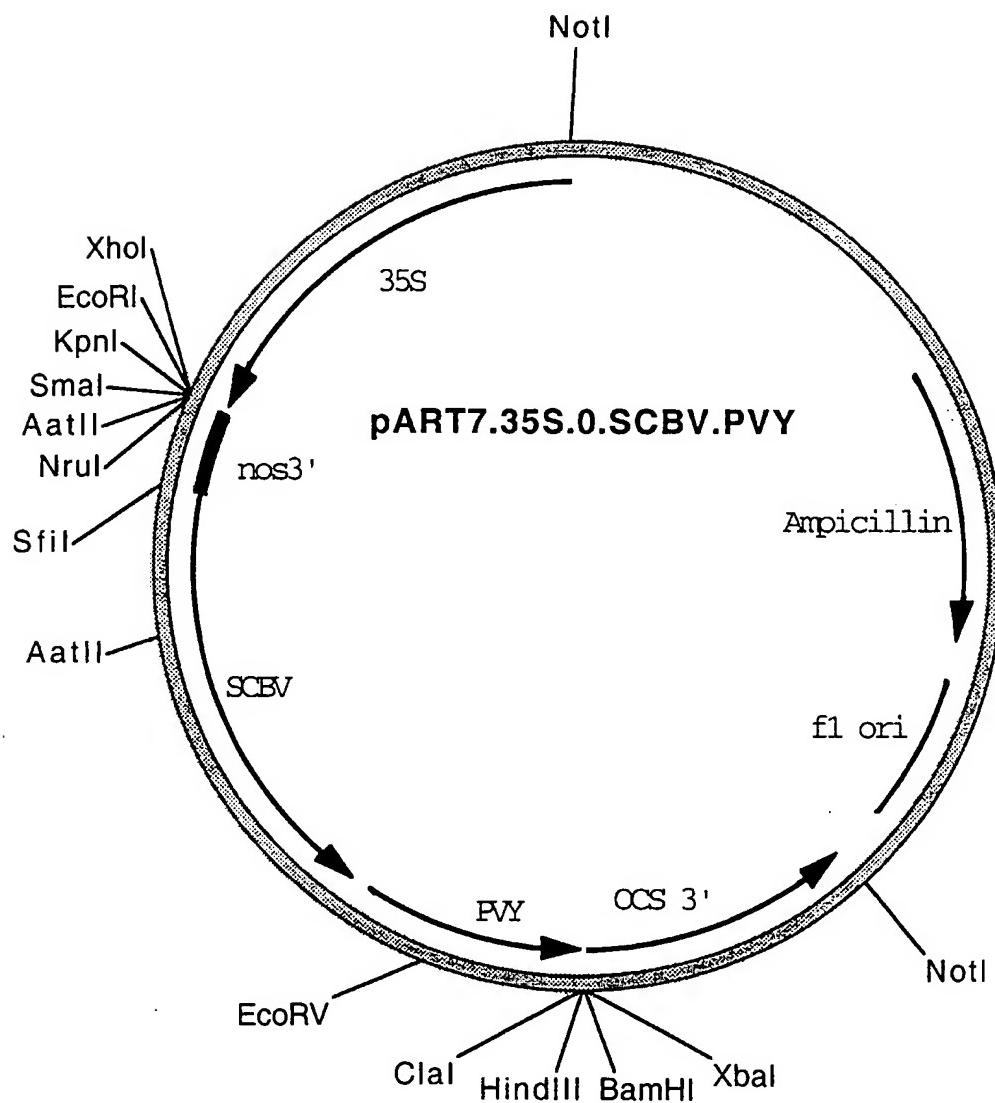
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## **FIGURE 54**

**FIGURE 55**

**FIGURE 56**

**FIGURE 57**

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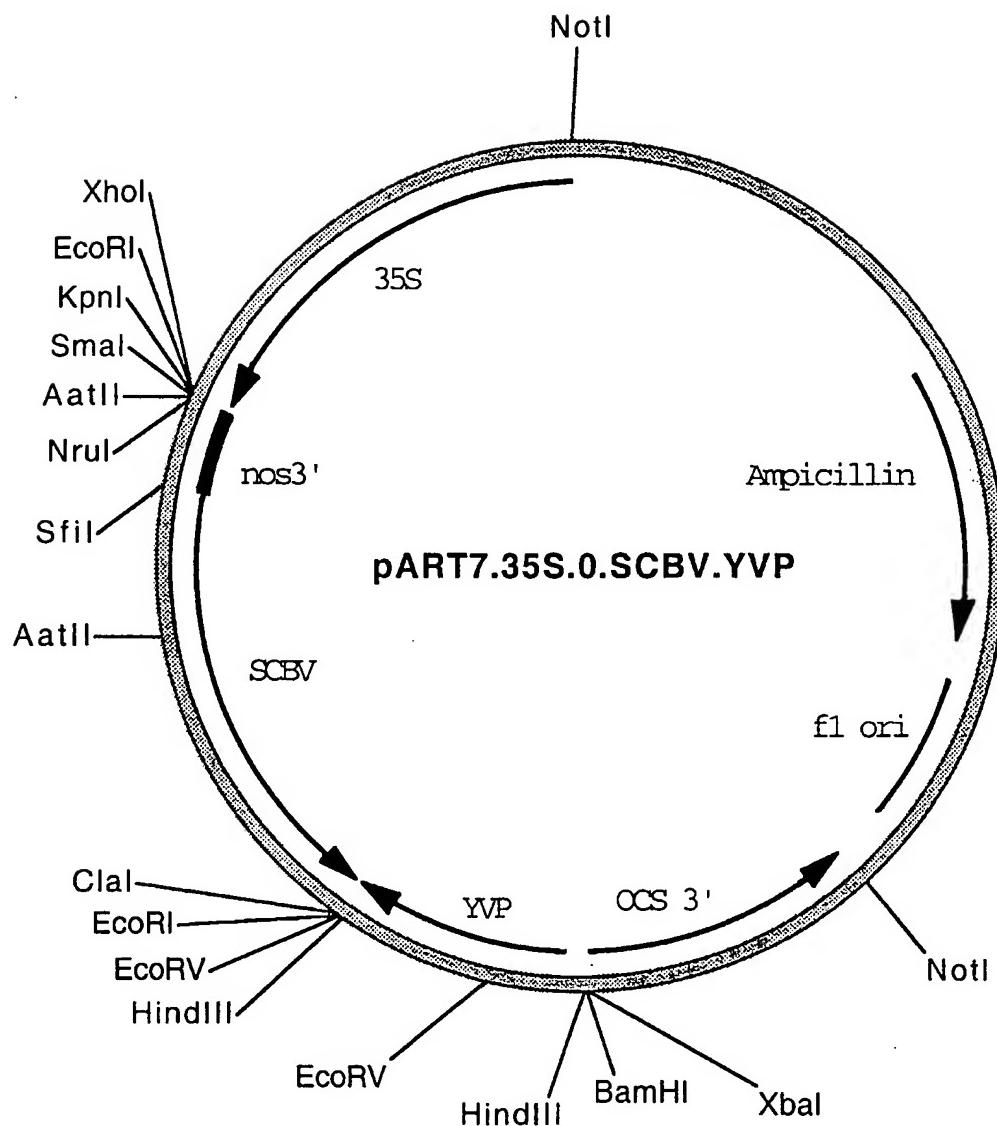


FIGURE 58

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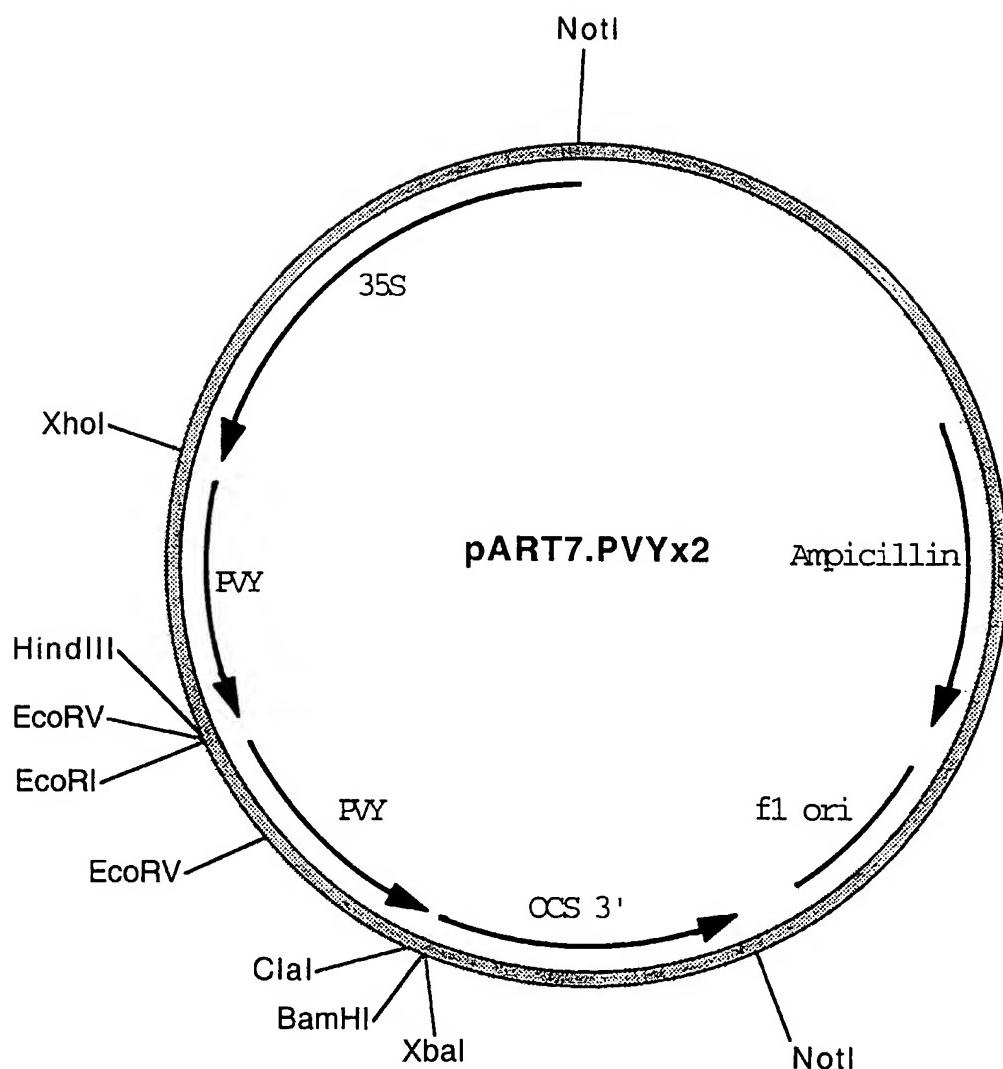


FIGURE 59

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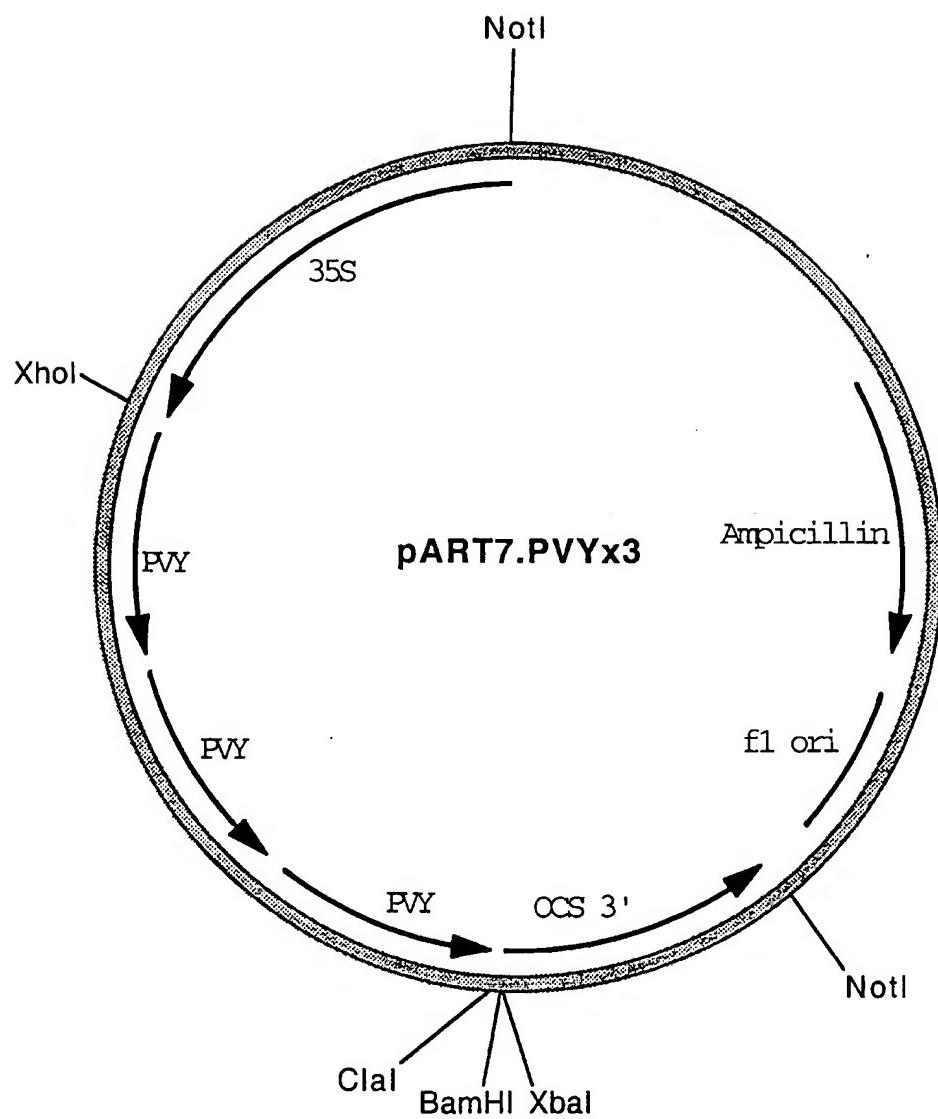
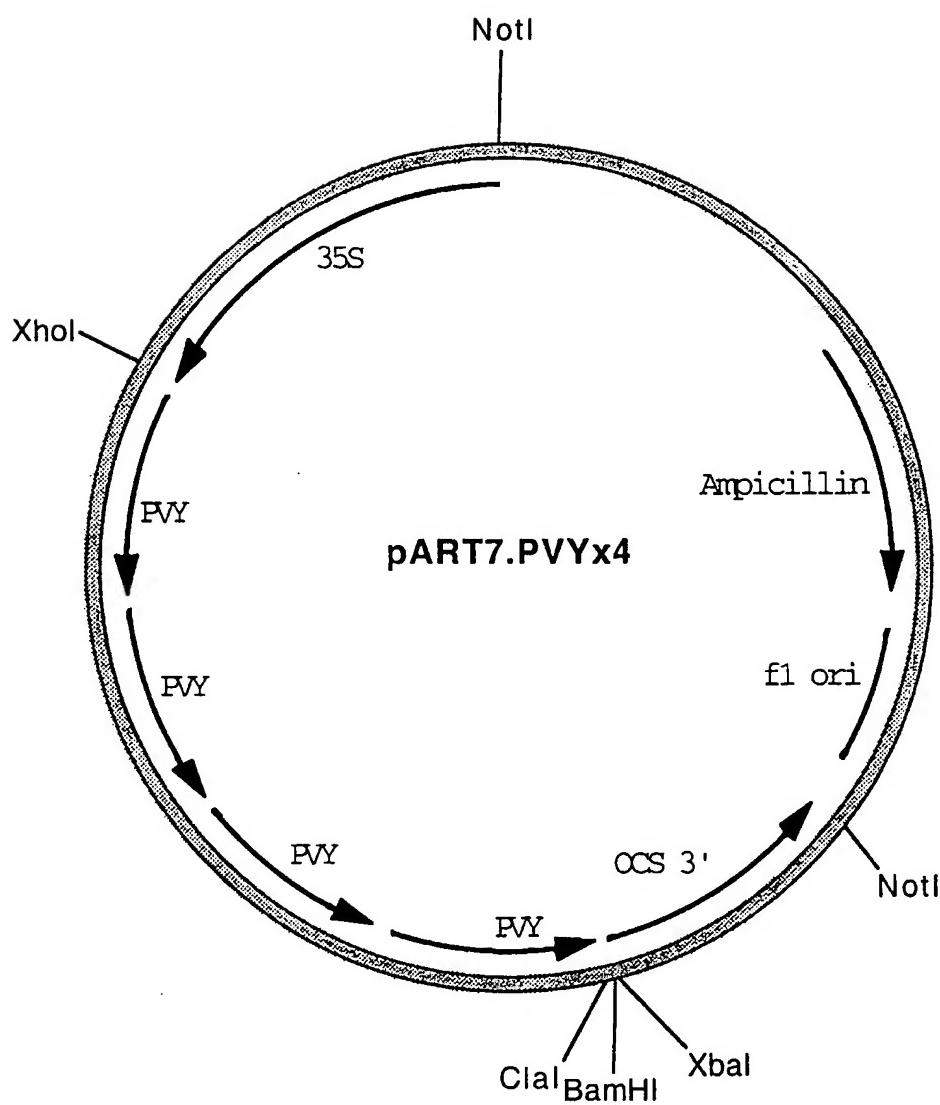


FIGURE 60

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**FIGURE 61**

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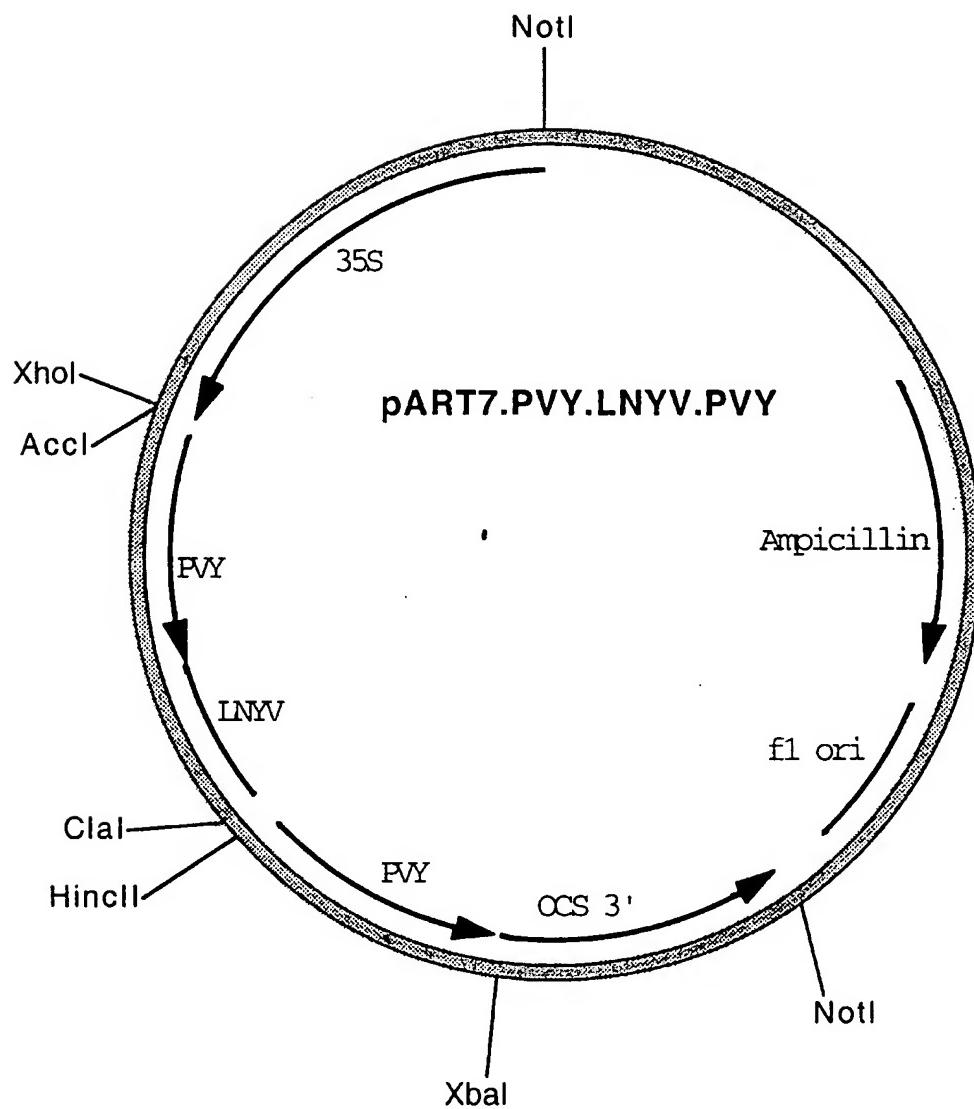
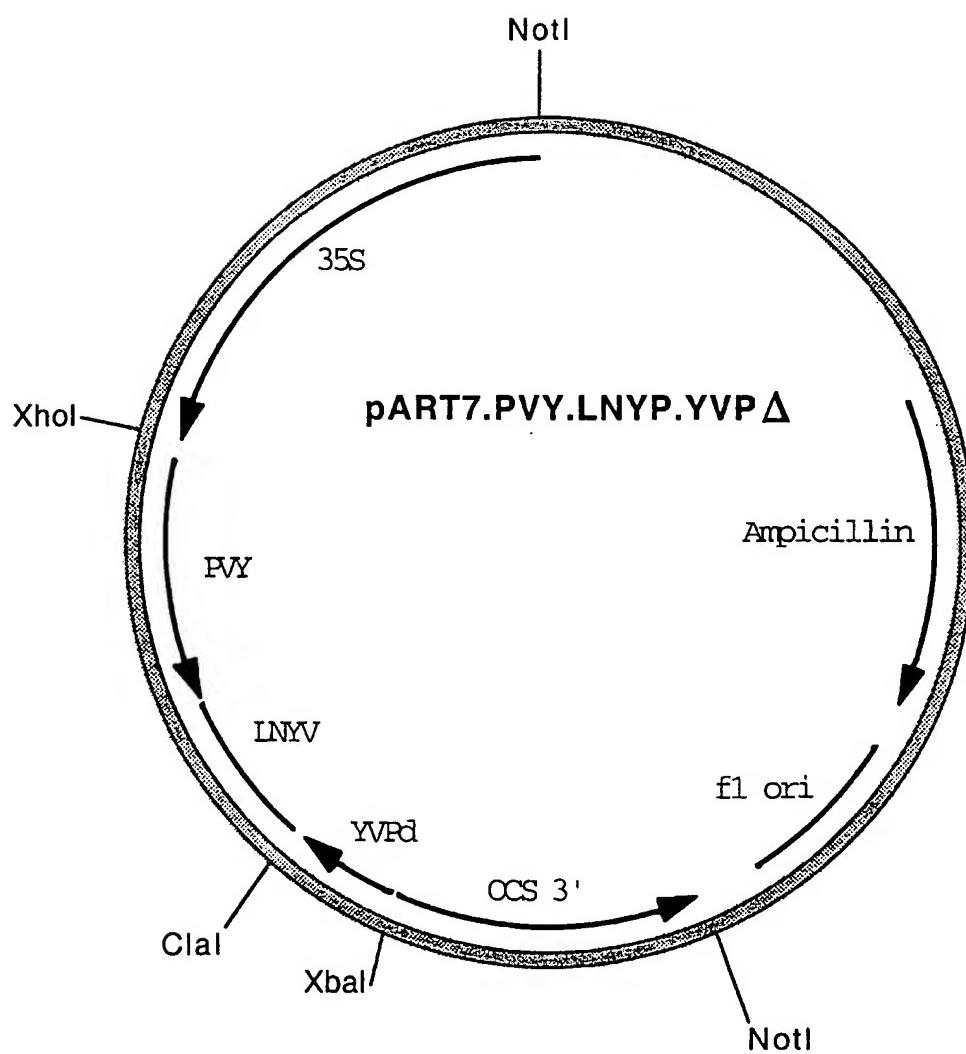


FIGURE 62

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**FIGURE 63**

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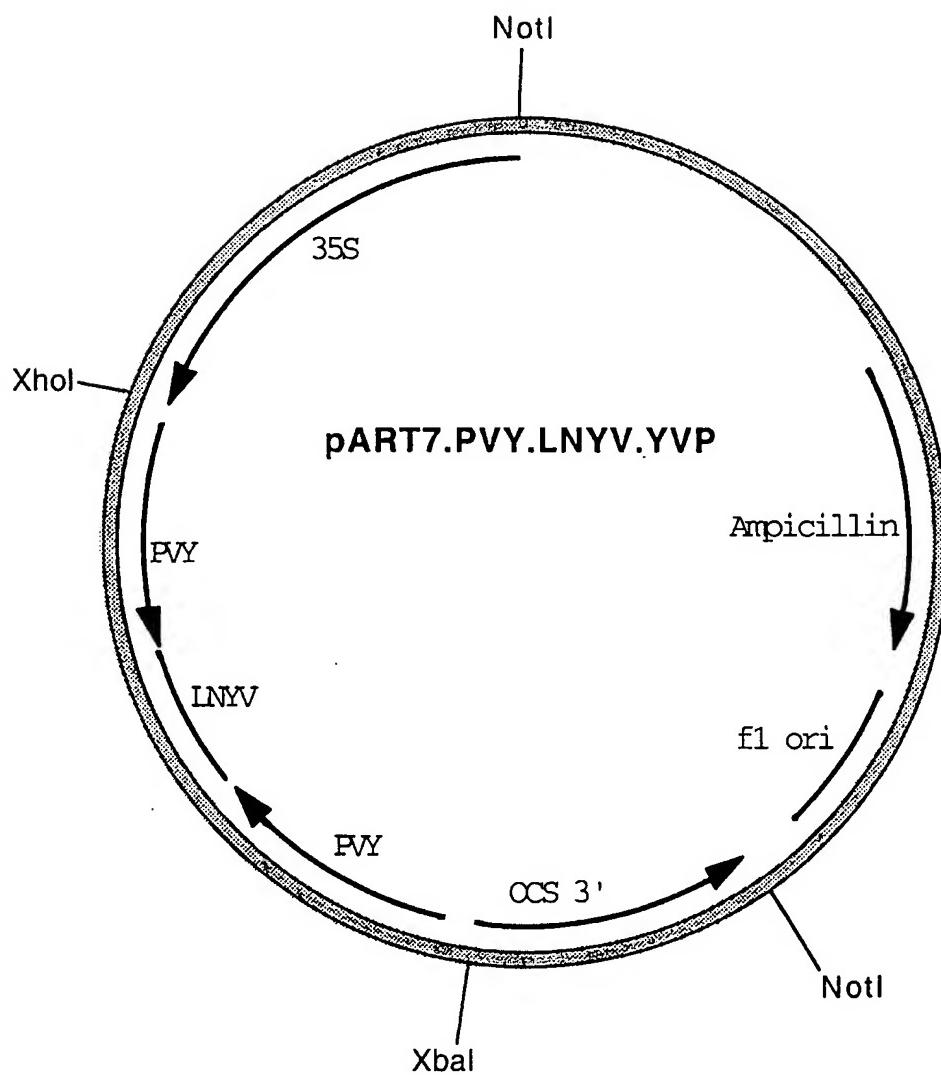


FIGURE 64

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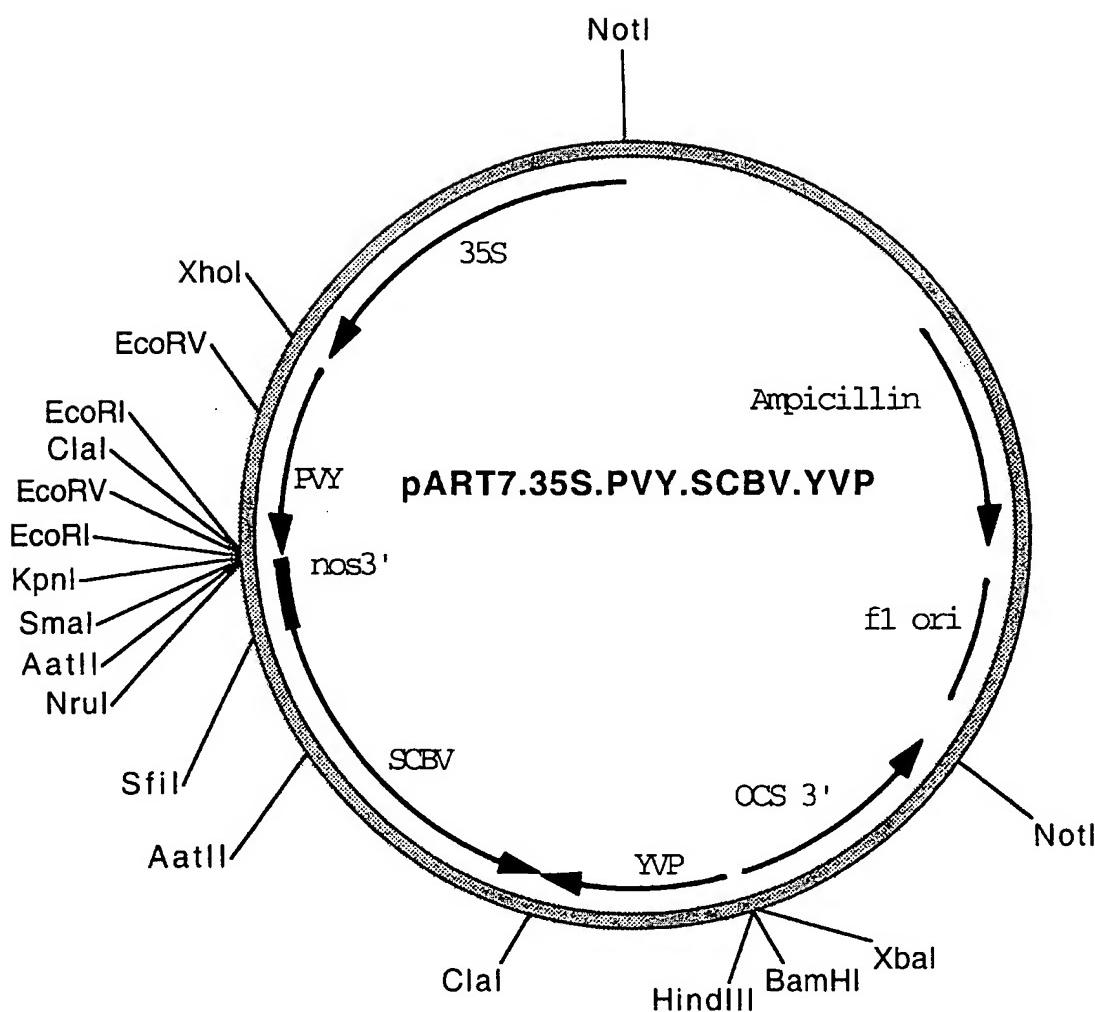


FIGURE 65

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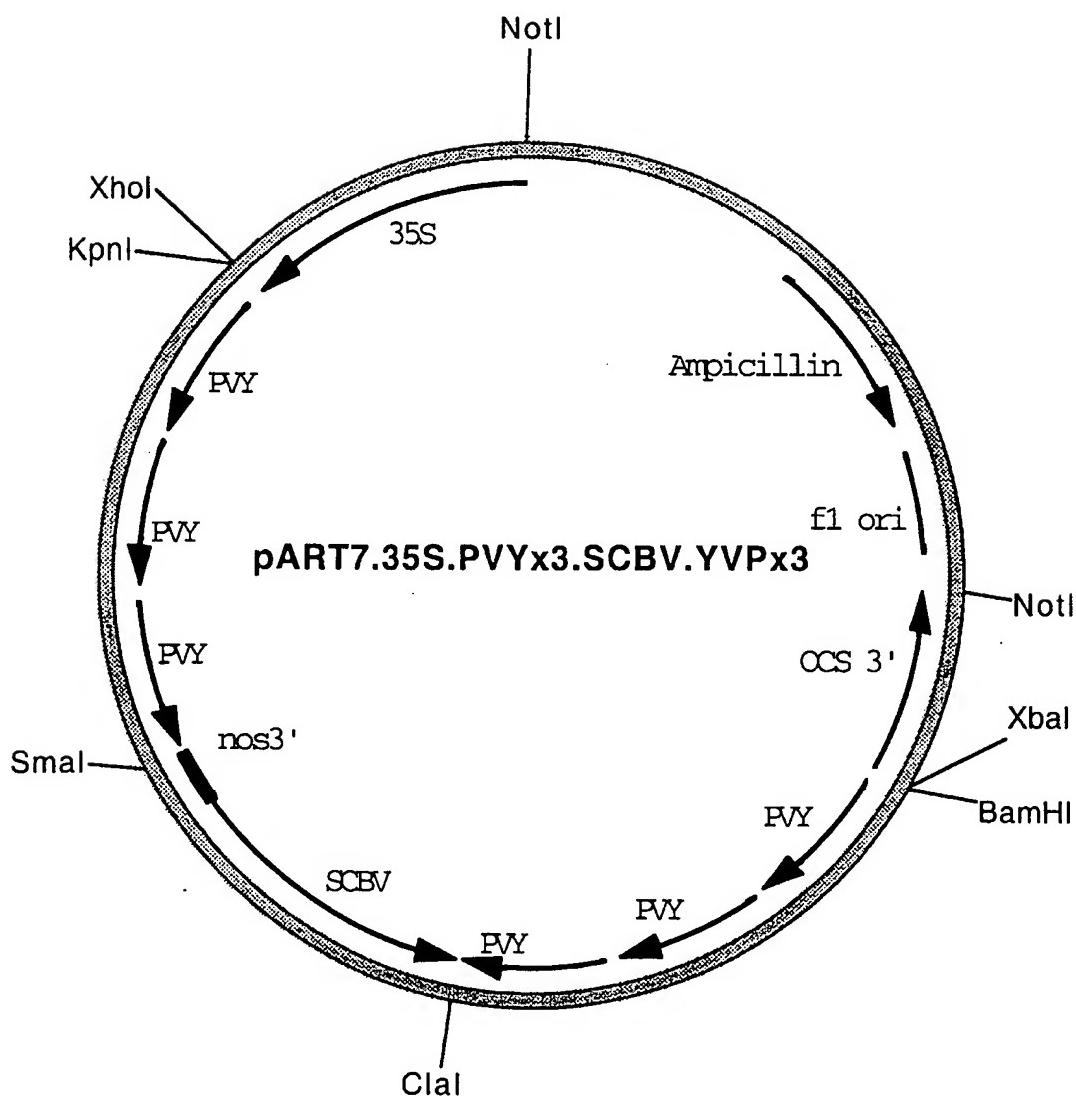
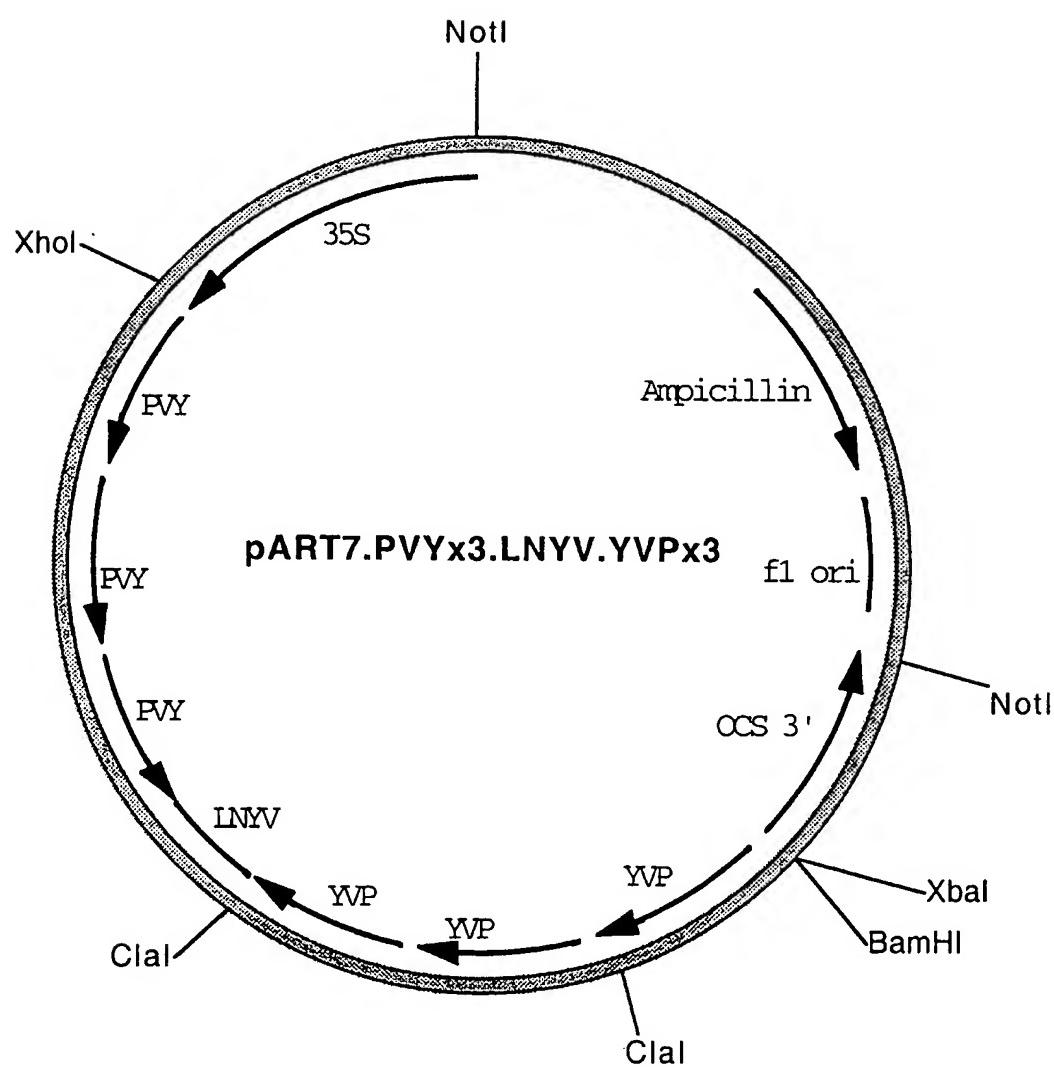
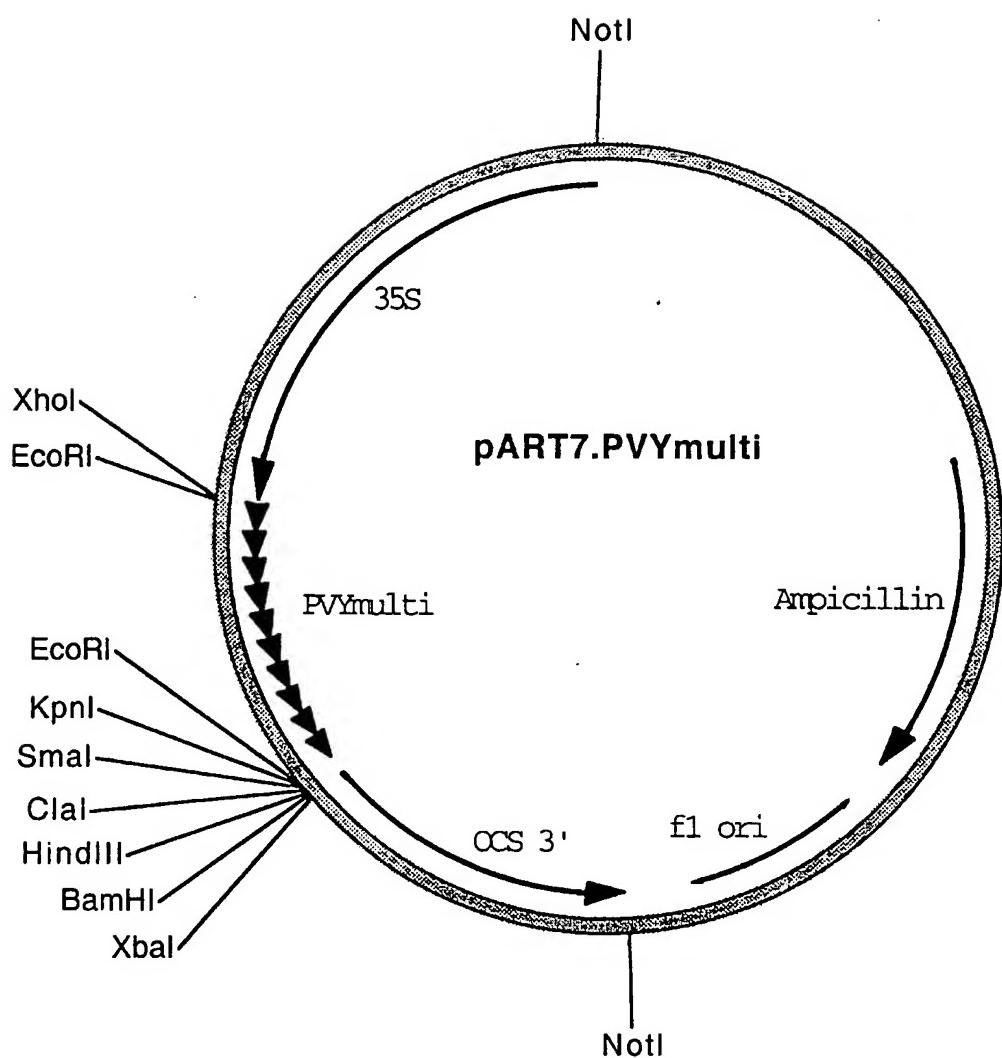


FIGURE 66

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**FIGURE 67**

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**FIGURE 68**

- 1 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: AgGene Australia Pty.Ltd and The Government of Queensland as represented by Queensland Department of Primary Industries

10

ii) TITLE OF INVENTION: Synthetic genes and genetic constructs comprising same I

iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

15

(A) ADDRESSEE: DAVIES COLLISON CAVE  
(B) STREET: 1 LITTLE COLLINS STREET  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA

20

(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

25

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:AU provisional  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES EL, JOHN E L

35

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777  
(B) TELEFAX: +61 3 9254 2770  
(C) TELEX: AA 31787

40

(2) INFORMATION FOR SEQ ID NO:1:

- 2 -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10

CGGCAGATCT AACAAATGGCA GGACAAATCG AGTACATC

38

(2) INFORMATION FOR SEQ ID NO:2:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 cccgggatcc tcgaaagaat cgtaccactt c

31

(2) INFORMATION FOR SEQ ID NO:3:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40

- 3 -

GGCGGGATCC TTAGAAAGAA TCGTACCA

29

(2) INFORMATION FOR SEQ ID NO:4:

5 (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15 CGGCAGATCT GGACAAATCG AGTACATC

28

(2) INFORMATION FOR SEQ ID NO:5:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGATCTGTAA ACGGCCACAA GTTCAG

26

30

(2) INFORMATION FOR SEQ ID NO:6:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

- 4 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCTTGT ACAGCTCGTC CATGCC

26

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCGACAATA AAATATCTTT ATTTTCATTA CATCTGTGTG TTGGTTTTTT GTGTGATTTT

60

TGCAAAAGCC TAGG

74

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCGACGTTT AGAGCAGAAG TAACACTTCC G

31

35

- 5 -

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCGGGGCTT AGTGTAAAAC AGGCTGAGAG

30

15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCGGGCAAA TCCCAGTCAT TTCTTAGAAA C

31

30 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

- 6 -

CGGCAGATCT AACAAATGGCA GGACAAATCG AGTACATC

38

(2) INFORMATION FOR SEQ ID NO:12:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 CCCGGGATCC TCGAAAGAAT CGTACCACTT C

31

(2) INFORMATION FOR SEQ ID NO:13:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

30

GGGC GGATCC TTAGAAAGAA TCGTACCAAC

29

(2) INFORMATION FOR SEQ ID NO:14:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

- 7 -

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 CGGCAGATCT GGACAAATCG AGTACATC

28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCGGGGCTT AGTGTAAAAC AGGCTGAGAG

30

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCGGGCAAA TCCCAGTCAT TTCTTAGAAA C

31

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU 99/00195

<b>A. CLASSIFICATION OF SUBJECT MATTER</b>		
Int Cl <sup>6</sup> : C12N 15/11		
According to International Patent Classification (IPC) or to both national classification and IPC		
<b>B. FIELDS SEARCHED</b>		
Minimum documentation searched (classification system followed by classification symbols) IPC (WPAT - WORLD PATENTS INDEX) AND CHEMICAL ABSTRACTS. KEYWORDS BELOW.		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched MEDLINE. KEYWORDS BELOW.		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WPAT, Medline, Chemical Abstracts. Keywords: homology, transcriptional, posttranscriptional, RNA mediated, epigenetic, silencing, cosuppression, virus resistance		
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	Cell, 96(3), 5 February 1999, Grant, "Dissecting the Mechanisms of Posttranscriptional Gene Silencing: Divide and Conquer", pages 303-6	1-49,57
X Y	Developmental Genetics, 22(1), 1998, Que et al., "Homology-Based Control of Gene Expression Patterns in Petunia Flowers", pages 100-9	<u>1-16,23,24,35,36,47-49,57</u> <u>17-22,25-34,37-49,57</u>
X Y	Plant Molecular Biology, 22(6), 1993, Assaad et al., "Epigenetic repeat-induced gene silencing (RIGS) in <i>Arabidopsis</i> ", pages 1067-85	<u>1-16,23,24,35,36,47-49,57</u> <u>17-22,25-34,37-49,57</u>
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C		<input checked="" type="checkbox"/> See patent family annex
<p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&amp;" document member of the same patent family</p>		
Date of the actual completion of the international search 30 April 1999	Date of mailing of the international search report <b>10 MAY 1999</b>	
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929	Authorized officer <b>CHRISTOPHER LUTON</b> Telephone No.: (02) 6283 2256	

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/AU 99/00195

<b>C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
<b>Category*</b>	<b>Citation of document, with indication, where appropriate, of the relevant passages</b>	<b>Relevant to claim No.</b>
P,X	The Plant Journal, 15(6), 1998, Hamilton et al., "A transgene with repeated DNA causes high frequency, post-transcriptional suppression of ACC-oxidase gene expression in tomato", pages 737-46	1-49,57
X	Annals of Botany, 79(1), 1997, Stam et al., "The Silence of Genes in Transgenic Plants", pages 3-12	1-49,57
X Y	Genetics, 147(3), 1997, Dorer and Henikoff, "Transgene Repeat Arrays Interact With Distant Heterochromatin and Cause Silencing in <i>cis</i> and <i>trans</i> ", pages 1181-90	<u>1-16,23,24,35,36,47-49,57</u> 17-22,25-34,37-49,57
X Y	Cell, 77(7), 1994, Dorer and Henikoff, "Expansions of Transgene Repeats Cause Heterochromatin Formation and Gene Silencing in <i>Drosophila</i> ", pages 993-1002	<u>1-16,23,24,35,36,47-49,57</u> 17-22,25-34,37-49,57
X	Plant Cell, Volume 8, 1996, Sijen et al., "RNA-Mediated Virus Resistance: Role of Repeated Transgenes and Delineation of Target Regions", pages 2277-94	1-49,57
P,X P,Y	WO, 98/53083 (ZENECA LIMITED) 26 November 1998	<u>1-16,23,24,35,36,47-49,57</u> 17-22,25-34,37-49,57

**INTERNATIONAL SEARCH REPORT**  
Information on patent family members

International application No.  
**PCT/AU 99/00195**

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member	
WO	98/53083	AU	74442/98
		GB	9710475

**END OF ANNEX**